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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:14:12 ; Search time 158.02 Seconds
(without alignments)
5.156 Million cell updates/sec

Title: US-09-281-760c-5
Perfect score: 63
Sequence: 1 GMLTYWRESK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :

A_Geneseq_1101.*
1: /SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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4: /SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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6: /SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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17: /SIDSI/gcgdata/geneseq/geneseqp/AA1996.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	11	21	AAV69585
2	63	100.0	11	21	AAV50879
3	63	100.0	20	18	AAW24098
4	63	100.0	124	18	AAW24097
5	63	100.0	312	21	AAV79995
6	63	100.0	341	21	AAW06208
7	63	100.0	417	18	AAW23067
8	63	100.0	426	17	AAW97753
9	59	93.7	22	21	AAV69587
10	54	85.7	11	21	AAV50882
11	43.5	69.0	12	21	AAV69592

12	41	65.1	351	13	AAW24251	Vaccinia virus B18
13	41	65.1	351	14	AAW41542	B15R product. Vac
14	41	65.1	574	21	AAV93969	Amino acid sequenc
15	41	65.1	562	22	AAW76658	Human lung tumour
16	41	65.1	583	17	AAW06891	Human activated le
17	41	65.1	583	17	AAW97230	Stem cell marker H
18	41	65.1	583	19	AAW47088	Activated leukocyt
19	40	63.5	11	21	AAV69581	Feline IGE-derived
20	40	63.5	11	21	AAV50881	Antibody 8H.8 bind
21	40	63.5	343	21	AAW06204	Platypos IGE heavy
22	38	60.3	107	22	AAW93603	Human anti-Rh(D) c
23	38	60.3	130	20	AAW97813	Bovine butyrophili
24	38	60.3	193	22	AAW60775	Gene 47 related pe
25	38	60.3	196	18	AAW10505	Alphalalipha2 regio
26	38	60.3	196	18	AAW10508	Alphalalipha2 regio
27	38	60.3	234	18	AAW10509	Soluble fused MHC
28	38	60.3	256	21	AAW68281	Class II alpha cha
29	38	60.3	256	21	AAV52935	Class II alpha cha
30	38	60.3	256	21	AAW58696	Class II alpha cha
31	38	60.3	441	18	AAW10507	Soluble fused MHC
32	38	60.3	448	18	AAW10513	Soluble fused MHC
33	38	60.3	458	17	AAW98907	Vector SCEL-deri
34	38	60.3	458	18	AAW29214	SCEL single chain
35	38	60.3	459	17	AAW98905	Vector SSCI-deri
36	38	60.3	459	17	AAW29212	SOCI single chain
37	38	60.3	494	22	AAW67480	A fusion protein c
38	38	60.3	500	17	AAW67480	Vector SCTL-deri
39	38	60.3	500	18	AAW29213	SOCI single chain
40	38	60.3	500	18	AAW27111	Single chain IAD/O
41	38	60.3	526	20	AAW97812	Bovine butyrophili
42	38	60.3	26926	22	AAW05396	Human titin (conn
43	37	58.7	860	14	AAW42862	Bovine MTP. Bos t
44	37	58.7	894	14	AAW42863	Human MTP. Homo s
45	37	58.7	894	14	AAW50007	Human MTP. Homo s
46	36	57.1	96	15	AAW54323	Anti-HIV gp120 imm
47	36	57.1	96	17	AAW01292	VL region of HIV n
48	36	57.1	96	21	AAV95144	Anti-gp120 antibod
49	36	57.1	96	21	AAV98253	Anti-gp120 antibod
50	36	57.1	108	20	AAW12352	Human 5' EST secre

ALIGNMENTS

RESULT 1	
ID	AAV69585 standard; peptide; 11 AA.
XX	
AC	AAV69585;
XX	
DT	19-APR-2000 (first entry)
XX	
DE	Canine IGE-derived peptide E3a.5, SEQ ID NO:10.
XX	
KW	Immunogenic; autoimmunity; IGE autoantibody; immunoglobulin E;
KW	allergy; canine; prophylaxis; treatment.
XX	
OS	Canis familiaris.
XX	
PN	EP955311-A2.
PD	10-NOV-1999.
XX	
PF	09-APR-1999; 99EP-0107020.
XX	
PR	09-APR-1998; 98US-0058332.
XX	
PR	30-MAR-1999; 99US-0281761.
XX	
PA	(IDEXX-) IDEXX LAB INC.
XX	
PI	Lawton R, Mermer B, Francoeur G;
DR	WPI; 2000-118182/11.

XX New peptides, useful for generating canine autoantibodies against
PT Immunoglobulin E (IGE) to treat allergic symptoms -
XX
XX
XX Claim 5; Page 5; 38pp; English.
XX
XX Sequences AAY69576-Y69586 and AAY69598-Y69599 represent peptides that may
CC be used to induce anti-IGE (immunoglobulin E) autoantibodies in a dog.
CC IGE is an important mediator of canine allergic responses, including Type
CC I immediate hypersensitivity. It is estimated that up to 30% of all dogs
CC suffer from allergies or allergy-related skin disorders, and allergic
CC dermatitis is thought to affect between 3 and 15% of dogs. Common canine
CC allergens include fleas, pollens, moulds and dust, with flea allergy
CC being the most frequent. Once IGE has been released in response to
CC allergen, the IGE binds to receptors on mast cells. The IGE molecules
CC can then become cross-linked, which induces the mast cells to release
CC histamine, which leads to the manifestation of allergic symptoms. The
CC peptides of the invention correspond to epitopes of canine IGE, or
CC conservative variations thereof, that are accessible in circulating IGE
CC but not in IGE bound to mast cells. The autoantibodies produced on
CC immunisation with such peptides therefore target only circulating IGE,
CC avoiding the possibility that they may cross-link bound IGE molecules,
CC which would exacerbate an ongoing allergic response even in the absence
CC of allergen. Anti-IGE autoantibody induction results in an immune
CC response that targets the IGE-expressing B cell, which affects IGE
CC synthesis by downregulating IGE production by B cells and/or targeting
CC the IGE-producing B cell for destruction. The peptides of the invention
CC are therefore useful for the treatment or prophylaxis of allergic
CC symptoms in a dog.
XX
XX
SQ Sequence 11 AA:

Query Match 100.0%; Score 63; DB 21; Length 11:
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GMLNTWYRESK 11
Db 1 gmlntwyresk 11

RESULT 2
AAY50879 standard; peptide; 11 AA.
XX ID AAY50879
XX AC AAY50879;
XX DT 24-FEB-2000 (first entry)
XX DE 8H.8 binding canine mimotope 1.
XX KM Canine; allergy; antibody 8H.8; IGE; B cell; mast cell; anti-allergy;
XX KW epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PS EP957111-A2.
XX PD 17-NOV-1999.
XX PF 09-APR-1999; 99EP-0107035.
XX PR 09-APR-1998; 98US-0058331.
XX PR 30-MAR-1999; 98US-0281760.
XX PA (IDEX-) IDEXX LAB INC.
XX PI Lawton R, Mermet B, Francoeur G;
XX DR WPI: 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy -

XX
XX Claim 10; Page 13; 30pp; English.
XX
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IGE, and which doesn't bind
CC to IGE when the IGE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IGE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
XX
XX
SQ Sequence 11 AA:

Query Match 100.0%; Score 63; DB 21; Length 11:
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GMLNTWYRESK 11
Db 1 gmlntwyresk 11

RESULT 3
AAW24098 standard; peptide; 20 AA.
XX ID AAW24098
XX AC AAW24098;
XX DT 21-NOV-1997 (first entry)
XX DE Canine immunoglobulin E peptide 1.
XX KM Immunoglobulin E; IGE; anti-canine IGE antibody; allergy; canine; dog.
XX OS Cantis famillaris.
XX PN JP09169795-A.
XX PD 30-JUN-1997.
XX PE 22-DEC-1995; 95JP-0334381.
XX PR 22-DEC-1995; 95JP-0334381.
XX PA (HITB) HITACHI CHEM CO LTD.
XX DR WPI: 1997-389423/36.
XX DR N-PSDB; AAT85647.
XX PT Canine immunoglobulin E peptide fragment and related DNA - useful
XX for the preparation of anti-canine immunoglobulin E antibody
XX PS Claim 2; Page 9; 12pp; Japanese.
XX CC AAW24098-106 are peptide fragments containing at least 5 continuous
CC amino acids of the partial canine immunoglobulin E (IGE) protein shown
CC in AAW24097. The peptides are used for the preparation of anti-canine
CC IGE antibody. The anti-canine IGE antibody can be used for the diagnosis
CC of canine allergies.
XX
XX
SQ Sequence 20 AA:

Query Match 100.0%; Score 63; DB 18; Length 20:
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GMLNTWYRESK 11
Db 1 gmlntwyresk 11

Db 3 gmltwyresk 13

RESULT 4

AAW24097 standard; peptide; 124 AA.

AAW24097;

21-NOV-1997 (first entry)

Partial canine immunoglobulin E protein.

Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.

Canis familiaris.

JP09169795-A.

30-JUN-1997.

22-DEC-1995; 95JP-0334381.

22-DEC-1995; 95JP-0334381.

(HITB) HITACHI CHEM CO LTD.

WPI: 1997-389423/36.

N-PSDB; AAT85646.

Canine immunoglobulin E peptide fragment and related DNA - useful

for the preparation of anti-canine immunoglobulin E antibody

Claim 1; Page 8; 12pp; Japanese.

This is a partial canine immunoglobulin E (IgE) protein. Peptide

fragments (AAW24098-106) containing at least five continuous amino acids

of this sequence are used for the preparation of anti-canine IgE

antibody. The anti-canine IgE antibody can be used for the diagnosis of

canine allergies.

Sequence 124 AA;

Query Match 100.0%; Score 63; DB 18; Length 124;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GMLTWTYRESK 11

13 gmltwtwyresk 23

15-MAY-2000 (first entry)

Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;

immunogenic; immunostimulatory; carrier protein; helper T cell epitope;

antibody; allergy; allergic disease; immunisation; anti-allergic;

anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

Canis sp.

WO9967293-A1.

29-DEC-1999.

21-JUN-1999; 99WO-US13959.

20-JUN-1998; 98US-0100287.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY, Walfield AM;

WPI: 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions

for immunization against allergy

Example 1; Page 66-68; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain

antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic

and anti-asthmatic properties. (I) induces polyclonal antibodies

specific for a target effector site on the epsilon-heavy chain of IgE,

and so preventing triggering and activation of mast cells and basophils

CC and downregulation of IgE synthesis. Conjugates, or fusion peptides,

containing (I) are used for active immunisation against IgE-mediated

allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy

dermatitis. Nucleic acids that encode these compounds are useful for

recombinant production of corresponding peptides or in DNA vaccines.

Conjugates of (I) that include a promiscuous T helper cell epitope

CC (functional in genetically diverse subjects), in addition to a B cell

target epitope, have increased immunogenicity and may include cyclic

CC constraints (disulfide bridge) to stabilise conformational features and

maximize cross-reactivity to the natural target. They induce safe

CC (non-anaphylactogenic) antibodies. AAY79994 to AAY80064 represent amino

acid sequences used in the exemplification of the present invention.

Sequence 312 AA;

Query Match 100.0%; Score 63; DB 21; Length 312;

Best Local Similarity 100.0%; Pred. No. 0.0031;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GMLTWTYRESK 11

143 gmltwtwyresk 153

22-NOV-2000 (first entry)

Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.

Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;

asthma; eczema; immunogenic peptide.

Chimeric - Didelphis virginiana.

Chimeric - Canis sp.

WO200025722-A2.

11-MAY-2000.

21-OCT-1999; 99WO-SE01896.

02-NOV-1998; 98US-0106652.

22-SEP-1999; 99US-0401636.

(RESI-) RESISTENTIA PHARM AB.

CC recombinant IGE using bacterial, yeast, mammalian, insect or
 CC viral systems. The IGE can be used in drug development (e.g.
 CC small molecule screening), assay development and anti-IGE
 CC antibody generation). Fragments of IGE can be used in vaccines
 CC or to prevent IGE-mediated hypersensitivity. The new sequence
 CC information permits targeted modulation of IGE-mediated immune
 CC responses.

XX
 SQ Sequence 426 AA;

Query Match 100.0%; Score 63; DB 17; Length 426;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMLTWYRESK 11
 Db 245 gmltwyresk 255

LXXR

RESULT 9

AA69587
 AAY69587 standard; peptide; 22 AA.

AC AAY69587;

DT 19-APR-2000 (first entry)

DE Peptide E3A.5-extended, SEQ ID NO:12.

KW Immunogenic; autoimmunity; IGE autoantibody; immunoglobulin E;
 KM allergy; canine; prophylaxis; treatment.

OS Canis familiaris.

PN EP955311-A2.

PD 10-NOV-1999.

PF 09-APR-1999; 99EP-0107020.

PR 09-APR-1998; 98US-0058332.

PR 30-MAR-1999; 99US-0281761.

PA (IDEX-) IDEXX LAB INC.

PI Lawton R, Mermer B, Francoeur G;

DR WPI: 2000-118182/11.

XX New peptides, useful for generating canine autoantibodies against
 XX Immunoglobulin E (IGE) to treat allergic symptoms -

XX Example 1; Page 16; 38pp; English.

CC The invention relates to peptides (AAY69576-Y69586, AAY69598-Y69599) that
 CC may be used to induce anti-IGE (immunoglobulin E) autoantibodies in a
 CC dog. IGE is an important mediator of canine allergic responses, including
 CC Type I immediate hypersensitivity. It is estimated that up to 30% of all
 CC dogs suffer from allergies or allergy-related skin disorders, and
 CC allergic dermatitis is thought to affect between 3 and 15% of dogs.
 CC Common canine allergens include fleas, pollens, moulds and dust, with
 CC flea allergy being the most frequent. Once IGE has been released in
 CC response to allergen, the IGE binds to receptors on mast cells. The IGE
 CC molecules can then become cross-linked, which induces the mast cells to
 CC release histamine, which leads to the manifestation of allergic symptoms.
 CC The peptides of the invention correspond to epitopes of canine IGE, or
 CC conservative variations thereof, that are accessible in circulating IGE
 CC but not in IGE bound to mast cells. The autoantibodies produced on
 CC immunisation with such peptides therefore target only circulating IGE,
 CC avoiding the possibility that they may cross-link bound IGE molecules,
 CC which would exacerbate an ongoing allergic response even in the absence
 CC of allergen. Anti-IGE autoantibody induction results in an immune

CC response that targets the IGE-expressing B cell, which affects IGE
 CC synthesis by downregulating IGE production by B cells and/or targeting
 CC the IGE-producing B cell for destruction. The peptides of the invention
 CC are therefore useful for the treatment or prophylaxis of allergic
 CC symptoms in a dog. Sequences AAY69587-Y69588 represent peptides used
 CC in exemplifications of the present invention.

XX
 SQ Sequence 22 AA;

Query Match 93.7%; Score 59; DB 21; Length 22;
 Best Local Similarity 90.9%; Pred. No. 0.00084;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GMLTWYRESK 11
 Db 1 gmltwyrese 11

RESULT 10

AA50882
 ID AAY50882 standard; peptide; 11 AA.

AC AAY50882;

DT 24-FEB-2000 (first entry)

DE Antibody 8H.8 binding substituted canine minotope 1.

KW Canine; allergy; antibody 8H.8; IGE; B cell; mast cell; anti-allergy;
 KM epitope; prophylaxis; treatment; minotope.

OS Synthetic.

PN EP957111-A2.

PD 17-NOV-1999.

PF 09-APR-1999; 99EP-0107035.

PR 09-APR-1998; 98US-0058331.

PR 30-MAR-1999; 99US-0281760.

PA (IDEX-) IDEXX LAB INC.

PI Lawton R, Mermer B, Francoeur G;

DR WPI: 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy -

XX Example 2; Page 13; 30pp; English.

CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IGE, and which doesn't bind
 CC to IGE when the IGE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IGE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAY50876-Y50900 represent peptide minotopes used in the method of the
 CC invention.

XX
 SQ Sequence 11 AA;

Query Match 85.7%; Score 54; DB 21; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0029;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GMLTWYRESK 11
 Db 1 gmltwyrese 11

Db 1 gmltwaresk 11

RESULT 11

ID AAY69592 standard; peptide: 12 AA.

XX AAY69592;

DT 19-APR-2000 (first entry)

DE Canine substituted IGE-derived peptide, SEQ ID NO:17.

KW IGE; immunoglobulin E; allergy; canine; mutant; muten; prophylaxis; treatment.

XX Canis familiaris.

OS Synthetic.

XX EP955311-A2.

XX 10-NOV-1999.

XX 09-APR-1999; 99EP-0107020.

XX 09-APR-1998; 98US-0058332.

XX 30-MAR-1999; 99US-0281761.

XX (IDEXX LAB INC.

PI Lawton R, Mermer B, Francoeur G;

XX MPI; 2000-118182/11.

PT New peptides, useful for generating canine autoantibodies against immunoglobulin E (IGE) to treat allergic symptoms -

XX Example 6; Page 19; 38pp; English.

XX The invention relates to peptides (AAY69576-Y69586, AAY69598-Y69599) that may be used to induce anti-IGE (immunoglobulin E) autoantibodies in a dog. IGE is an important mediator of canine allergic responses, including Type I immediate hypersensitivity. It is estimated that up to 30% of all dogs suffer from allergies or allergy-related skin disorders, and allergic dermatitis is thought to affect between 3 and 15% of dogs. Common canine allergens include fleas, pollens, moulds and dust with flea allergy being the most frequent. Once IGE has been released in response to allergen, the IGE binds to receptors on mast cells. The IGE molecules can then become cross-linked, which induces the mast cells to release histamine, which leads to the manifestation of allergic symptoms. The peptides of the invention correspond to epitopes of canine IGE, or conservative variations thereof, that are accessible in circulating IGE but not in IGE bound to mast cells. The autoantibodies produced on immunisation with such peptides therefore target only circulating IGE, avoiding the possibility that they may cross-link bound IGE molecules, which would exacerbate an ongoing allergic response even in the absence of allergen. Anti-IGE autoantibody induction results in an immune response that targets the IGE-expressing B cell, which affects IGE synthesis by downregulating IGE production by B cells and/or targeting the IGE-producing B cell for destruction. The peptides of the invention are therefore useful for the treatment or prophylaxis of allergic symptoms in a dog. Sequences AAY69590-Y69592 represent peptides compared with peptide AAY69584 in binding studies with the anti-canine IGE monoclonal antibody 8H.8 in an exemplification of the present invention.

XX Sequence 12 AA;

Query Match 69.0%; Score 43.5; DB 21; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.22; Mismatches 1; Gaps 1;
Matches 10; Conservative 0; Indels 1;

QY 1 GMLTW-VRESK 11
Db 1 gmltwaresk 12

RESULT 12

ID AAR24251 standard; protein: 351 AA.

XX AAR24251;

DT 23-NOV-1992 (first entry)

DE Vaccinia virus B18r protein.

KW Recombinant; polyvalent vaccine; interleukin binding; IL-2; IL-6; multiple pathogens.

XX Human vaccinia virus.

XX Key Location/Qualifiers

FH Disulfide-bond 73..129 /note="Intradomain disulphide bridge"

FT Disulfide-bond 172..221 /note="Intradomain disulphide bridge"

FT Disulfide-bond 272..333 /note="Intradomain disulphide bridge"

FT Region 117..119 /note="N-linked carbohydrate addition site"

FT Region 172..174 /note="N-linked carbohydrate addition site"

FT Region 251..253 /note="N-linked carbohydrate addition site"

FT Region 269..271 /note="N-linked carbohydrate addition site"

FT Region 321..323 /note="N-linked carbohydrate addition site"

XX WO9207944-A.

XX 14-MAY-1992.

XX 28-OCT-1991; 91WO-GB01882.

XX 26-OCT-1990; 90GB-0023352.

XX (LYNX-) LYNXVALE LTD.

XX Smith GL;

XX WPI; 1992-183679/22.

XX N-PSDB: AAC25097.

PT New vaccinia vector genes and expression products - useful in diagnosis and treatment of inflammatory conditions

XX Disclosure; Fig 1c; 73pp; English.

XX The sequence is that of the vaccinia virus B18r protein which is involved in the binding of interleukin (IL)-2 and/or IL-6 and in preventing them from reaching their natural receptors, hence the inflammatory response is diminished and viral replication is enhanced. Its gene sequence may be inactivated or all or part of it deleted to allow greater attenuation of the virus, enhanced immunogenicity of the recombinant vaccinia virus and/or provide sites for the insertion of heterologous genes. This recombinant vaccinia virus may be used as a live vaccine in both human and veterinary medicine. See also AAR24250 and AAR24252.

XX Sequence 351 AA;

Query Match 65.1%; Score 41; DB 13; Length 351;

Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 3 NLTWYRESK 11
|:||||::|
Db 182 nltwykdk 190

RESULT 13

AA041542
ID AA041542 standard; Protein: 351 AA.

XX AC AA041542;

XX DT 25-MAR-1994 (first entry)

XX DE B15R product.

XX B15R: interleukin-1 beta; IL-1; diagnosis; kit; inflammation;
KW rheumatoid arthritis; septic shock; cancer; fever; bowel disease;
KM graft versus host disease; diabetes; expression; B15R.

XX Vaccinia virus.

XX Key Location/Qualifiers

XX Peptide 9..19

XX /label= possible_sig_peptide

XX Modified-site 117..119

XX /label= possible_N-linked_carbohydrate_site

XX Modified-site 184..186

XX /label= possible_N-linked_carbohydrate_site

XX Modified-site 261..263

XX /label= possible_N-linked_carbohydrate_site

XX Modified-site 269..271

XX /label= possible_N-linked_carbohydrate_site

XX Modified-site 321..323

XX /label= possible_N-linked_carbohydrate_site

XX Disulfide-bond 73

XX /label= possible_linking_site

XX Disulfide-bond 129

XX /label= possible_linking_site

XX Disulfide-bond 172

XX /label= possible_linking_site

XX Modified-site 221

XX /label= possible_linking_site

XX Disulfide-bond 272

XX /label= possible_linking_site

XX Disulfide-bond 333

XX /label= possible_linking_site

XX WO9318153-A.

PD 16-SEP-1993.

XX 05-MAR-1993; 93WO-GB00460.

XX 05-MAR-1992; 92GB-0004780.

XX (SMIT/) SMITH G L.

XX Smith GL;

XX WPI: 1993-303467/38.

XX N-PSDB: AA046244.

XX New vaccinia virus B15R nucleotide sequence - used to prepare

XX prods. to treat conditions with interleukin-I beta mediated

XX symptoms

XX Disclosure: Fig 1C; 91pp; English.

XX The sequence (AA046243) encodes a protein that specifically binds to

XX IL-1-beta and can be used to block the activity of IL-1-beta and treat

CC

CC

CC

CC

CC

CC

CC IL-1-beta mediated conditions. The sequence can also be used as part
CC of a kit to detect and measure IL-1B. The sequence (AA046244) encodes a
CC similar protein and recombinant vvs in which expression of B15R and
CC B15R is inactivated. To introduce restriction sites close to the
CC initiator methionine of B15R, a PCR copy of the 5' region of the
CC ORF was constructed using primers (AA046241-42).

XX Sequence 351 AA;

Query Match 65.1%; Score 41; DB 14; Length 351;

Best Local Similarity 55.6%; Pred. No. 24;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLTWYRESK 11

Db 182 nltwykdk 190

RESULT 14

AA041542
ID AA041542 standard; Protein: 574 AA.

XX AC AA041542;

XX DT 03-OCT-2000 (first entry)

XX Amino acid sequence of a partial rat antigen Ag2117.

XX Antigen: Ag2117; pancreatic cell; monoclonal antibody; surface antigen.

XX Rattus sp.

XX WO200037503-A1.

XX 29-JUN-2000.

XX 22-DEC-1999; 99WO-US30741.

XX 22-DEC-1998; 98US-0218539.

XX (RAVE-) RAVEN BIOTECHNOLOGIES INC.

XX Mather JP, Bald LM, Roberts PR, Stephan JF;

XX WPI: 2000-452179/39.

XX N-PSDB: AAA57480.

XX Immunizing a host mammal to produce population of monoclonal antibodies

XX that bind to antigens of specific cell type comprises introducing

XX viable cells with serum-free surfaces -

XX Example 10; Fig 10; 61pp; English.

XX The present sequence represents rat antigen Ag2117. The antigen is

XX representative of pancreatic cell lines. The antibody that recognises

XX Ag2117 was identified using the method of the invention. The

XX specification describes a method for immunizing a host mammal to produce

XX a population of monoclonal antibodies that bind to antigens

XX representative of a specific cell type that are heterologous to the

XX host mammal. The method comprises introducing into the mammal intact

XX and viable cells with surfaces which are free of serum. The methods

XX are useful for producing populations of antibodies that bind to antigens

XX representative of a specific cell type, specifically antibodies that

XX are tissue-selective, sub-tissue selective or cell-type specific. These

XX antibodies facilitate the identification of novel antigens and the

XX delineation of the combination of surface antigens on a specific cells

XX type. The antibodies or hybridomas produced using the methods have

XX diagnostic and therapeutic applications.

XX Sequence 574 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 65.1%; Score 41; DB 21; Length 574;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX 3 NLTWYRESK 11
DB 167 nltwyrngk 175
XX
RESULT 15
ID AAB76858 standard; Protein: 582 AA.
XX AAB76858;
XX AAB76858;
XX 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related protein sequence SPO ID NO:334.
XX
XX Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
XX Lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
XX Cytostatic; antisense inhibition.
XX Homo sapiens.
XX
XX WO200100828-A2.
XX 04-JAN-2001.
XX
XX 30-JUN-2000; 2000MO-US18061.
XX
XX 30-JUN-1999; 99US-0346492.
XX 15-OCT-1999; 99US-0419356.
XX 17-DEC-1999; 99US-0466867.
XX 30-DEC-1999; 99US-0476300.
XX 06-MAR-2000; 2000US-0519642.
XX 22-MAR-2000; 2000US-0533077.
XX 10-APR-2000; 2000US-0546259.
XX 27-APR-2000; 2000US-0560406.
XX 05-JUN-2000; 2000US-0589184.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Bangur CS, Iodes MJ, Fanger GR, Vedvick TS, Carter D;
XX Reiter MW, Mannion J;
XX MPI: 2001-071488/08.
XX
XX Lung tumor-associated proteins and the nucleic acids that encode them,
XX useful for preventing, diagnosing and treating lung cancer -
XX
XX Example 1; Page 262-264; 436pp; English.
XX
XX The present invention describes immunogenic portions of lung tumour-
XX associated proteins (I) and the nucleic acids (NAs) that encode them.
XX (I) have cytostatic activity and can be used in gene therapy, antisense
XX inhibition and in vaccines. The NAs and the lung tumour-associated
XX proteins they encode may be used in the prevention, treatment and
XX diagnosis of diseases associated with their inappropriate expression,
XX especially lung cancers. For example, the NAs may be administered to
XX treat diseases by rectifying mutations or deletions in a patient's genome
XX that affect the activity of the protein by expressing inactive proteins
XX or to supplement the patient's own production of (I). Additionally, the
XX NAs may be used to produce the lung tumour associated protein, according
XX to standard recombinant DNA methodology. Conversely, antisense NA
XX molecules may be administered to down regulate protein expression by
XX binding with the cells own genes and preventing their expression. The NA
XX and complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar NA sequences in
XX samples, and hence which patients may be in need of treatment for lung
XX cancer. The (I) may be used as antigens in the production of antibodies
XX and in assays to identify modulators (agonists and antagonists) of the
XX expression and activity of the protein. AAF68083 to AAF68878 and

CC AAB76848 to AAB76878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
CC of the present invention.
XX
XX Sequence 582 AA;
SQ
Query Match 65.1%; Score 41; DB 22; Length 582;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX 3 NLTWYRESK 11
DB 166 nltwyrngk 174
XX
RESULT 16
ID AAM06891 standard; Protein: 583 AA.
XX AAM06891;
XX AAM06891;
XX 18-MAR-1997 (first entry)
XX
XX Human activated leukocyte-cell adhesion molecule ALCAM.
XX
XX Activated leukocyte-cell adhesion molecule; ALCAM; CD6 ligand;
XX thymic epithelial cell; inflammation; allograft rejection;
XX neurodegenerative disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..27
XX /label= Sig-peptide
XX 28..583
XX /label= Mat-protein
XX 28..527
XX /label= Extracellular domain
XX /note= "the extracellular domain can be subdivid"
XX 528..551
XX /label= Transmembrane domain
XX 552..583
XX /label= Extracellular domain
XX 91
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX 95
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX 167
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX 258
XX /label= Asn, Ser
XX /note= "variation owing to polymorphism in HL60
XX and T-cell derived clones"
XX 265
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX 301
XX /label= Met, Thr
XX /note= "variation owing to polymorphism in HL60
XX and T-cell derived clones"
XX 306
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX 337
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX 361
XX /label= Glycosylation
XX /note= "putative N-glycosylation site"
XX

FT	Modified-site	457	/label= Glycosylation
FT	Modified-site	480	/note= "putative N-glycosylation site"
FT	Modified-site	499	/label= Glycosylation
FT	Modified-site	499	/note= "putative N-glycosylation site"
FT	Modified-site	499	/label= Glycosylation
FT	Modified-site	499	/note= "putative N-glycosylation site"
PN	MO9634880-A1.		
XX	07-NOV-1996.		
XX	29-APR-1996.	96MO-US06010.	
PF	01-MAY-1995.	95US-0432016.	
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.		
PA	(UYDU-) UNIT DUKE.		
XX	Azucio A, Bowen MA, Haynes BF, Marguardt H, Patel D;		
XX	WPI: 1996-506097/50.		
DR	N-PSDB: AAT46075.		
XX	CD6 ligands present on surface of thymic epithelial cells - used to		
FT	develop prods. for treating e.g. inflammation, organ allograft		
PT	rejection or neurodegenerative diseases		
XX	Example 4: Fig 29; 112pp; English.		
PS	Human activated leukocyte cell adhesion molecule (AA006891) or ALCAM		
XX	is a CD6 ligand present on the surface of thymic epithelial cells,		
CC	monocytes, activated T-cells, and other cells. Its amino acid		
CC	sequence was deduced from cDNA clones (AAT46075) obtcd. from HU60		
CC	and T-cell lines. ALCAM polypeptides can be produced, e.g. as a		
CC	fusion proteins, in transformed host cells. They are useful for		
CC	inhibiting CD6/CD6 interactions between cells and to screen for		
CC	agents that modulate this interaction. Inhibitors can be used to		
CC	treat e.g. inflammation, multiple sclerosis, inflammatory uveitis,		
CC	rheumatoid arthritis, T-cell mediated vasculitis syndromes, organ		
CC	allograft rejection and neurodegenerative diseases.		
XX	Sequence 583 AA;		
SO			
XX	Query Match	65.1%;	Score A1; DB 17; Length 583;
XX	Best Local Similarity	66.7%;	Pred. No. 42;
XX	Matches 6; Conservative 1;	Mismatches 2;	Indels 0; Gaps 0;
XX	3 NLTWYRESK 11		
XX	1:11111 1		
XX	167 nltwyngk 175		
DB			
XX	RESULT 17		
ID	AA097230		
XX	AA097230 standard; Protein; 583 AA.		
AC	AA097230;		
XX	08-OCN-1996 (first entry)		
DT	Stem cell marker HCAPPro.1.		
XX	Stem cell marker; haematopoietic cell antigen; HCA; HCASeq.1;		
XX	HCAPPro.1.		
OS	Homo sapiens.		
XX	EP716146-A2.		
XX			

[illegible]

FT Misc-difference 258 /label= Asn, Ser
 FT /note= "encoded by AAT (polymorphism in nucleotide
 FT sequence"
 FT Modified-site 265 /note= "N-glycosylated"
 FT MISC-difference 301 /label= Met, Thr
 FT /note= "encoded by AYC (polymorphism in nucleotide
 FT sequence)"
 FT Modified-site 306 /note= "N-glycosylated"
 FT Modified-site 337 /note= "N-glycosylated"
 FT Modified-site 361 /note= "N-glycosylated"
 FT MISC-difference 447 /note= "encoded by CAR"
 FT Modified-site 457 /note= "N-glycosylated"
 FT Modified-site 480 /note= "N-glycosylated"
 FT Modified-site 499 /note= "N-glycosylated"
 FT Modified-site /note= "N-glycosylated"
 FT MO9803551-A1.
 FT 29-JAN-1998.
 FT 17-JUL-1997: 97MO-US12511.
 FT 18-JUL-1996: 96US-0684594.
 FT (BRIM) BRISTOL-MYERS SQUIBB CO.
 FT (UYDU-) UNIV DUKE.
 FT
 FT Anuffo A, Bowen MA, Haynes BF, Marguardt H, Patel D;
 FT Stadelk AW;
 FT WPI: 1998-120703/11.
 FT N-PSDB: AAV13954.
 FT
 FT Activated leukocyte-cell adhesion molecule (ALCAM), a new CD6 ligand
 FT - useful for screening compounds which inhibit interaction of ALCAM
 FT and CD6 ligand antibodies
 FT
 FT Claim 3: Fig 29; 130pp; English.
 FT
 FT This polypeptide is a human CD6 ligand (see AAMA7088), designated
 FT activated leukocyte-cell adhesion molecule (ALCAM), that is present
 FT on the surface of thymic epithelial cells, monocytes, activated
 FT T cells and a variety of other cells. Its amino acid sequence was
 FT deduced from cDNA clones (see AAV13954) isolated from human T cell
 FT and HL60 cDNA libraries. It is the human homologue of chicken
 FT BBN, and shows homology to neuroilin, RAGE and MC18. Anti-CD6
 FT ligand antibodies, or their binding fragments, are useful for
 FT inhibiting binding of CD6 present on the surface of a first cell
 FT to that present on a second cell. CD6 ligands and anti-CD6 ligand
 FT antibodies are also useful in screening test compounds for the
 FT ability to inhibit binding of CD6 ligand to an anti-CD6 ligand
 FT antibody (all claimed).
 FT
 FT Sequence 583 AA:
 SO

Query Match 65.1%; Score 41; DB 19; Length 583;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6: Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 NUTWYRESK 11
 I:|||||
 Db 167 nltwyngk 175

RESULT 19
 AAV69591
 ID AAV69591 standard: peptide: 11 AA.
 AC AAV69591;
 DT 19-APR-2000 (first entry)
 DE Feline IgE-derived peptide, SEQ ID NO:16.
 KW IgE; immunoglobulin E; feline; allergy; canine; prophylaxis; treatment.
 OS Fells catus.
 XX
 XX EP955311-A2.
 XX 10-NOV-1999.
 XX 09-APR-1999; 99EP-0107020.
 XX 09-APR-1998; 98US-0058332.
 XX 30-MAR-1999; 99US-0281761.
 XX (IDEX-) IDEXX LAB INC.
 XX Lawton R, Mermer B, Francoeur G;
 XX WPI: 2000-118182/11.
 XX
 XX New peptides, useful for generating canine autoantibodies against
 XX immunoglobulin E (IgE) to treat allergic symptoms -
 XX
 XX Example 6: Page 19; 38pp; English.
 XX
 XX The invention relates to peptides (AAV69576-Y69586, AAV69598-Y69599) that
 XX may be used to induce anti-IgE (immunoglobulin E) autoantibodies in a
 XX dog. IgE is an important mediator of canine allergic responses, including
 XX Type I immediate hypersensitivity. It is estimated that up to 30% of all
 XX dogs suffer from allergies or allergy-related skin disorders, and
 XX allergic dermatitis is thought to affect between 3 and 15% of dogs.
 XX Common canine allergens include fleas, pollens, moulds and dust, with
 XX flea allergy being the most frequent. Once IgE has been released in
 XX response to allergen, the IgE binds to receptors on mast cells to
 XX release histamine, which leads to the manifestation of allergic symptoms.
 XX The peptides of the invention correspond to epitopes of canine IgE, or
 XX but not in IgE bound to mast cells. The autoantibodies produced on
 XX immunisation with such peptides therefore target only circulating IgE,
 XX avoiding the possibility that they may cross-link bound IgE molecules,
 XX which would exacerbate an ongoing allergic response even in the absence
 XX of allergen. Anti-IgE autoantibody induction results in an immune
 XX response that targets the IgE-expressing B cell, which affects IgE
 XX synthesis by downregulating IgE production by B cells and/or targeting
 XX the IgE-producing B cell for destruction. The peptides of the invention
 XX are therefore useful for the treatment or prophylaxis of allergic
 XX symptoms in a dog. Sequences AAV69590-Y69592 represent peptides
 XX compared with peptide AAV69584 in binding studies with the anti-canine
 XX IgE monoclonal antibody 8H.8 in an exemplification of the present
 XX invention.
 XX
 XX Sequence 11 AA:
 SO

Query Match 63.5%; Score 40; DB 21; Length 11;
 Best Local Similarity 70.0%; Pred. No. 0.8;
 Matches 7: Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GMLTWYRES 10
 I:|||||
 Db 1 gmltweren 10

RESULT 20
 AAY50881
 ID AAY50881 standard; peptide: 11 AA.
 XX
 AC AAY50881;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Antibody 8H.8 binding feline mimotope 1.
 XX
 KW Canine; allergy; antibody 8H.8; IGE; B cell; mast cell; anti-allergy;
 KM epitope; prophylaxis; treatment; mimotope.
 XX
 OS Synthetic.
 XX
 PN EP957111-A2.
 PD 17-NOV-1999.
 XX
 PF 09-APR-1999; 99EP-0107035.
 XX
 PR 09-APR-1998; 98US-0058331.
 XX 30-MAR-1999; 99US-0281760.
 XX
 PA (IDEX-) IDEXX LAB INC.
 PI Lawton R, Mermer B, Francoeur G;
 DR WPI: 2000-040833/04.
 XX
 DT Blinding proteins used for treatment or prophylaxis of canine allergy -
 XX
 PS Example 2; Page 13; 30pp; English.
 XX
 CC This invention describes a novel binding protein which specifically
 CC binds to native canine free or B-cell bound IGE, and which doesn't bind
 CC to IGE when the IGE is bound to mast cells. The peptide products of the
 CC invention have anti-allergic activity. The antibodies bind to defined
 CC epitopes on free or B-cell bound IGE molecules which have an important
 CC role in allergic reaction. The specific binding proteins are used to
 CC produce a pharmaceutical composition, preferably with a diluent, which
 CC can be used for prophylaxis or treatment of canine allergy.
 CC AAT50876-Y50900 represent peptide mimotopes used in the method of the
 CC invention.
 CC
 CC Sequence 11 AA;
 SQ

Query Match 63.5%; Score 40; DB 21; Length 11;
 Best Local Similarity 70.0%; Pred. No. 0.8;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GNNLTWYRES 10
 |||||
 Db 1 gnnltwsren 10

RESULT 21
 AAB06204
 ID AAB06204 standard; protein: 343 AA.
 XX
 AC AAB06204;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Platypus IGE heavy chain constant regions 2, 3 and 4.
 XX
 KW Platypus; immunoglobulin E; IGE; vaccination; infection; allergy;
 KM asthma; eczema; immunogenic peptide.
 XX
 OS Ornithorhynchus anatinus.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 1..343
 FT /label= OTHER
 FT /note= "Xaa=unknown"
 XX
 PN WO200025722-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 21-OCT-1999; 99WO-SE01896.
 XX
 PR 02-NOV-1998; 98US-0106652.
 XX 22-SEP-1999; 99US-0401636.
 XX
 PA (RESI-) RESISTENTIA PHARM AB.
 XX
 PI Hellman LT;
 XX
 DR WPI: 2000-365342/31.
 XX
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals -
 XX
 PS Disclosure; Fig 2; 50pp; English.
 XX
 CC The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2, 3 and 4 of the platypus IGE. It was used to
 CC construct a number of immunogenic peptides which consisted of regions of
 CC IGE from different mammals, which appear to cause a stronger polyclonal
 CC anti-self IGE response than peptides consisting of the same regions from
 CC one mammal. Immunogenic peptides, particularly those consisting of
 CC different heavy chain constant regions, can be used for vaccination
 CC in humans, against bacterial and viral infections and allergies, such
 CC as asthma, fur, pollen and food allergies and eczema.
 CC
 CC Sequence 343 AA;
 SQ

Query Match 63.5%; Score 40; DB 21; Length 343;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GNNLTWYRES 10
 |||||
 Db 163 gnevtwsres 172

RESULT 22
 AAG93603
 ID AAG93603 standard; protein: 107 AA.
 XX
 AC AAG93603;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) chain I16 protein sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX
 OS Homo sapiens.
 XX
 PN US6255455-B1.
 XX
 PD 03-JUL-2001.
 XX
 PF 29-JAN-1999; 99US-0240274.
 XX
 PR 11-OCT-1996; 96US-0028550.
 XX 10-APR-1998; 98US-0081380.
 XX 27-JUN-1997; 97US-0884045.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.

XX Siegel DL;
 XX WPI: 2001-388931/41.
 DR N-PSDB; AAH68660.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine -
 PS Claim 1: Column 44: 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (1) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93659. (1) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (1) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAG8615 to AAG8726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification
 CC of the present invention.
 XX
 SO Sequence 107 AA:
 Query Match 60.3%; Score 38; DB 22; Length 107;
 Best Local Similarity 50.0%; Pred. No. 22;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GMLTYWRES 10
 DB 29 gfnlnwygqt 38
 RESULT 23
 AAG97813
 ID AAG97813 standard; Protein: 130 AA.
 XX
 AC AAG97813;
 XX
 DT 21-MAY-1999 (first entry)
 XX
 DE Bovine butyrophillin Igt domain.
 XX
 KW Butyrophillin; cattle; bovine; multiple sclerosis; diagnosis;
 KW vaccine; transgenic animal; food; dairy product; milk.
 XX
 OS Bos taurus.
 XX
 PN WO9905162-A1.
 XX
 PD 04-FEB-1999.
 XX
 PF 22-JUL-1998; 98WO-US15062.
 XX
 PR 22-JUL-1997; 97US-0053376.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 PI Linington C, Mather IH;
 XX
 FI WPI: 1999-142845/12.
 XX
 CC New modified butyrophillin - not cross-reactive with myelin
 CC oligodendrocyte glycoprotein, useful in dairy products, vaccines,
 CC and assays for susceptibility to multiple sclerosis
 XX
 PS Disclosure; Page 38-39: 53pp; English.
 CC This polypeptide comprises the intermediate-type immunoglobulin
 CC like domain (Igt of bovine butyrophillin (BRN, see AAG97812), a major

CC component of the milk fat globule membrane and member of the
 CC immunoglobulin (Igt) superfamily. The Igt domain of BRN has a high
 CC degree of identity with the Igt domain of myelin/oligodendrocyte
 CC glycoprotein (MOG, see AAG97817). Immunisation with exogenous BRN
 CC induces the production of antibodies which cross-react with
 CC endogenous MOG, and this predisposes animals to pathological
 CC autoimmune responses such as multiple sclerosis (MS). The
 CC invention is directed to methods of modifying the BRN protein to
 CC eliminate sequences that elicit this immune response to MOG, e.g.
 CC by removing or modifying the Igt domain of a non-human BRN (nBRN)
 CC in a dairy product, or by producing a humanised chimeric BRN
 CC composed of an exoplasmic domain comprising a human Igt domain and
 CC nBRN (preferably bovine) Igt1 domain, and a cytoplasmic domain
 CC comprising a nBRN (preferably bovine) B30.2 region. The invention
 CC includes genetic manipulation of the endogenous BRN gene of an
 CC animal such that the human Igt domain is introduced into the
 CC germ line of the animal, and the animal expresses the humanised
 CC protein in its milk. Dairy products including modified nBRN or
 CC chimeric BRN are also provided. A diagnostic method for detecting
 CC susceptibility to MS in a patient from injecting bovine BRN is
 CC claimed. Identification of a human patient at risk of developing a
 CC pathogenic autoimmune response to MOG on exposure to nBRN is also
 CC possible, by screening the patient with a test for polypeptides in the
 CC gene with domains which are at least 50% identical to nBRN Igt
 CC domains (claimed). Peptides derived from nBRN and constructs
 CC based on nucleic acids encoding nBRN, are used as vaccines to
 CC induce immunological tolerance to nBRN in humans (claimed).
 XX
 SO Sequence 130 AA:
 Query Match 60.3%; Score 38; DB 20; Length 130;
 Best Local Similarity 66.7%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GMLTYWRE 9
 DB 34 gmelirwfre 42
 RESULT 24
 AAB60775
 ID AAB60775 standard; peptide: 193 AA.
 XX
 AC AAB60775;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Gene 47 related peptide #1.
 XX
 KW Secreted protein; gene therapy; vaccine; cancer; leukemia;
 KW autoimmune disease; allergy; inflammation; graft rejection;
 KW hyperproliferation; cardiovascular; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200076531-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US15137.
 XX
 PR 11-JUN-1999; 99US-0138625.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 XX
 FI WPI: 2001-071148/08.
 XX
 CC Nucleic acids encoding 47 human secreted polypeptides, useful for
 CC preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 CC disease and diabetic retinopathy -

XX disclosure; Page 523-524; 525pp; English.
 PS
 CC The present invention relates to 26 secreted human proteins. The
 CC proteins may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate polypeptide expression.
 CC For example, they may be used in gene therapy or in vaccines.
 CC Typical of diseases which are potentially treatable are cancers
 CC (including leukemia), autoimmune diseases, allergies, inflammation,
 CC graft rejection, hyperproliferation, cardiovascular diseases
 CC (particularly critical limb ischemia and coronary disease) and any
 CC involving abnormal angiogenesis, neurodegeneration and/or
 CC infectious diseases.
 CC
 SQ Sequence 193 AA:

Query Match 60.3%; Score 38; DB 22; Length 193;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 GMMTWYRE 9
 |||||
 19 gmeirwre 27

RESULT 25
 AAM10505
 ID AAM10505 standard; Protein; 196 AA.
 XX

AC AAM10505;

DT 12-SEP-1997 (first entry)

DE Alpha1pha2 region of Class II NOD mouse MHC (IAG7).

XX Soluble; fusion: major histocompatibility complex; MHC; region;
 KM heterodimer; complex; alpha2; antigen; binding groove; tolerance;
 KM autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
 KM antagonist; T cell; anergy; presenting cell; NOD mouse;
 KM Class II; alpha1.

XX Mus spp.

PN WO9640944-A2.

PD 19-DEC-1996.

PF 07-JUN-1996; 96MO-0510102.

27-OCT-1995; 95US-0005964.

07-JUN-1995; 95US-0480002.

07-JUN-1995; 95US-0482133.

07-JUN-1995; 95US-0483241.

PA (ANER-) ANERGEN INC.

PI (ZYMO) ZYMOGENETICS INC.

DR Deshpande S, Gross JA, Kindsvogel W, Reich EP, Sheppard PO;

DR N-PSDB; AAT00698.

XX Novel fused major histocompatibility complex:antigenic peptide

PT complex - useful to induce tolerance to an autoantigen-related

PT disease e.g. insulin-dependent diabetes mellitus

XX Example 3; Pages 132-133; 142pp; English.

CC to associate with a peptide binding groove of the MHC molecule,
 CC linked in frame to the DNA encoding the 2nd domain by a DNA
 CC encoding a 5-25 residue linker. The complex can be used to induce
 CC immunological tolerance in adults susceptible to, or suffering from
 CC an autoantigen related disease, e.g. insulin dependent diabetes
 CC mellitus (IDDM), by antagonising the binding of particular T cells
 CC and antigen presenting cells, to induce anergy (immunological
 CC non-responsiveness) in the targeted T cell. As the heterodimers and
 CC corresponding antigen are permanently linked into a single chain,
 CC obviating the requirement for complex heterodimer truncation or
 CC formation, the complex eliminates inefficient and non-specific
 CC peptide loading.
 CC
 SQ Sequence 196 AA:

Query Match 60.3%; Score 38; DB 18; Length 196;
 Best Local Similarity 60.0%; Pred. No. 42;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 MNLTWYRESK 11
 :||| |
 Db 121 initwlrnsk 130

Search completed: April 21, 2002, 10:14:14
 Job time: 184 sec

Sun Apr 21 10:51:23 2002

us-09-281-760c-5.open.rag

Page 14



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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:46:37 ; Search time 26.44 Seconds
(without alignments)
19.611 Million cell updates/sec

Title: US-09-281-760C-4

Sequence: 1 TLELYRM 7

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 47201

Minimum DB seq length: 0
Minimum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

Database :

A.Geneseq.1101.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
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21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	21	AA169584
2	35	100.0	7	21	AA150878
3	23	65.7	7	22	AAU03292
4	22	62.9	7	20	AA148904
5	22	62.9	7	21	AA121922
6	22	62.9	7	22	AA160498
7	20	60.0	6	21	AA1603076
8	20	57.1	4	21	AA1603078
9	20	57.1	5	21	AA1603077
10	20	57.1	6	21	AA1603075
11	19	54.3	5	18	AA112480

12	19	54.3	6	13	AA124624	Immunomodulatory p
13	19	54.3	6	13	AA124650	Immunomodulatory p
14	19	54.3	6	19	AA187231	Peptide determined
15	19	54.3	6	19	AA187232	Peptide determined
16	19	54.3	6	19	AA175344	Hexapeptide #9 bin
17	19	54.3	6	19	AA175276	Hexapeptide #9 bin
18	19	54.3	6	22	AA163041	Amino acid sequenc
19	19	54.3	7	13	AA124651	Immunomodulatory p
20	19	54.3	7	13	AA124652	Immunomodulatory p
21	19	54.3	7	13	AA124654	Immunomodulatory p
22	19	54.3	7	13	AA190639	S. solifaticus tr
23	18	51.4	5	17	AA109684	Cyclic pentapeptid
24	18	51.4	5	21	AA136778	HRC-beta1 variant
25	18	51.4	7	17	AA194522	GLU4 synthetic pep
26	18	51.4	7	20	AA143592	Amino acids 498-50
27	18	51.4	7	20	AA149785	Elastolytic peptid
28	18	51.4	7	20	AA149795	Elastolytic peptid
29	17	48.6	4	19	AA147950	AE101 analogue eff
30	17	48.6	5	17	AA105258	Cyclic pentapeptid
31	17	48.6	5	17	AA102183	Residues 359-363 o
32	17	48.6	5	18	AA112518	Interleukin-6 anta
33	17	48.6	5	19	AA147949	AE101 analogue eff
34	17	48.6	5	20	AA139643	Zea mays pathogen
35	17	48.6	5	21	AA136775	HRC-beta1 variant
36	17	48.6	5	21	AA136777	HRC-beta1 variant
37	17	48.6	5	21	AA193426	Peptide motif from
38	17	48.6	5	21	AA183328	Peptide motif of s
39	17	48.6	6	11	AA1804740	Deduced sequence a
40	17	48.6	6	15	AA156261	Peptide correspond
41	17	48.6	6	19	AA187227	Peptide determined
42	17	48.6	6	19	AA187228	Peptide determined
43	17	48.6	6	19	AA187229	Peptide determined
44	17	48.6	6	19	AA187230	Peptide determined
45	17	48.6	6	19	AA187231	AE101 analogue eff
46	17	48.6	6	20	AA141948	Rheumatoid arthrit
47	17	48.6	7	17	AA185590	Human glycoprotein
48	17	48.6	7	19	AA148887	AE101 analogue eff
49	17	48.6	7	20	AA148887	Membrane dipeptida
50	17	48.6	7	20	AA195149	Peptide ligand bin

ALIGNMENTS

RESULT 1	
AA169584	
ID	AA169584 standard; peptide: 7 AA.
AC	AA169584;
XX	
DT	19-APR-2000 (first entry)
XX	
DE	Immunogenic peptide seq ID NO:9, for anti-IGE autoantibody generation.
XX	
KW	Immunogenic; autoimmunity; IGE autoantibody; immunoglobulin E;
KW	allergy; canine; prophylaxis; treatment.
XX	
OS	Synthetic.
XX	
PN	EP95311-A2.
XX	
PD	10-NOV-1999.
XX	
PF	09-APR-1999; 99EP-0107020.
XX	
PR	09-APR-1998; 98US-0058332.
XX	
PR	30-MAR-1999; 99US-0281761.
XX	
PA	(IDEXX-) IDEXX LAB INC.
XX	
PI	Lawton R, Wermer B, Francoeur G;
XX	
DR	WPI; 2000-118182/11.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:53:50 ; Search time 26.68 Seconds
(Without alignments)
30.540 Million cell updates/sec

Title: US-09-281-760C-5
Perfect score: 63
Sequence: 1 GNNLWYRESK 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 132282

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: /SIDSI/gcgdata/geneseq/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/AA1982.DAT:*
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22: /SIDSI/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	11	21	AAV69585
2	63	100.0	11	21	AAV50879
3	54	85.7	11	21	AAV50882
4	40	63.5	11	21	AAV69591
5	40	63.5	11	21	AAV50881
6	33	52.4	10	18	AAW22686
7	30	47.6	7	21	AAV69580
8	30	47.6	7	21	AAV50880
9	30	47.6	9	17	AAW49652
10	30	47.6	10	20	AAW40646
11	30	47.6	10	21	AAW29985

12	29	46.0	7	19	AAW53900
13	28	44.4	9	17	AAW49505
14	27	42.9	6	18	AAW22699
15	27	42.9	9	22	AAU15304
16	27	42.9	10	18	AAW22688
17	27	42.9	10	18	AAW22687
18	26	41.3	8	15	AAW60424
19	26	41.3	8	15	AAW60447
20	26	41.3	10	22	AAW87239
21	26	41.3	11	17	AAW05276
22	26	41.3	11	19	AAW54288
23	25	39.7	7	20	AAV04349
24	25	39.7	8	15	AAW60425
25	25	39.7	8	15	AAW60446
26	25	39.7	8	15	AAW60431
27	25	39.7	9	20	AAV55436
28	25	39.7	9	20	AAV46859
29	25	39.7	10	17	AAW12590
30	25	39.7	10	20	AAV40648
31	25	39.7	10	20	AAV40649
32	25	39.7	10	20	AAV40650
33	25	39.7	10	21	AAW23987
34	25	39.7	10	21	AAW23988
35	25	39.7	10	21	AAW23989
36	24	38.1	6	17	AAW90506
37	24	38.1	6	20	AAV35233
38	24	38.1	6	20	AAW85714
39	24	38.1	6	21	AAW86979
40	24	38.1	6	22	AAW69385
41	24	38.1	8	14	AAW36082
42	24	38.1	8	15	AAW60437
43	24	38.1	8	20	AAV03896
44	24	38.1	8	22	AAJ00475
45	24	38.1	8	22	AAJ00972
46	24	38.1	8	22	AAJ01677
47	24	38.1	8	22	AAW78520
48	24	38.1	9	18	AAW45164
49	24	38.1	9	18	AAW37010
50	24	38.1	9	18	AAW37010

ALIGNMENTS

AAV69585	1	AAV69585 standard; peptide; 11 AA.
ID	AAV69585;	
AC	AAV69585;	
DT	19-APR-2000 (first entry)	
DE	Canine IgE-derived peptide E3a.5, SEQ ID NO:10.	
XX	Immunogenic; autoimmunity; IgE autoantibody; immunoglobulin E;	
KW	allergy; canine; prophylaxis; treatment.	
OS	Canis familiaris.	
PN	EP955311-A2.	
PD	10-NOV-1999.	
XX	09-APR-1999; 99EP-0107020.	
PF	09-APR-1998; 98US-0058332.	
PR	30-MAR-1999; 99US-0281761.	
XX	(INDEX-) IDEXX LAB INC.	
PA	Lawton R, Mermer B, Francoeur G;	
PI	WPI; 2000-118182/11.	
DR		

Interleukin-1 rece
Human leucocyte an
BSW17 peptide mime
Schizophrenia-rasso
BSW17 peptide mime
BSW17 peptide mime
BSW17 peptide mime
Antiproliferative
Antiproliferative
Breast-cancer asso
PERB11-5D peptide.
Cytoshesin 1 PH dom
Dengue antigenic p
Antiproliferative
Antiproliferative
Antiproliferative
HLA binding plu-1
Immunogenic peptid
SH2 binding peptid
S2 derivative #10,
S2 derivative #11,
S2 derivative #12,
Scaffold protein S
Scaffold protein S
Scaffold protein S
Hypriodoma ATCC HB-
ATCC HB 11884 mono
Peptide derived fr
Human haematopiet
Grand fir monoterp
Hepatitis C virus
Hepatitis C virus
Antiproliferative
Predicted binding
Hepatitis C virus
Hepatitis C virus
Hepatitis C virus
HIV-1 gp 41 enhanc
Human cartilage gl
TRP-2 derived pote

XX New peptides, useful for generating canine autoantibodies against
PT Immunoglobulin E (IgE) to treat allergic symptoms -
XX
XX Claim 5; Page 5; 38pp; English.
XX
XX Sequences AAY69576-Y69586 and AAY69598-Y69599 represent peptides that may
CC be used to induce anti-IgE (immunoglobulin E) autoantibodies in a dog.
CC IgE is an important mediator of canine allergic responses, including Type
CC I immediate hypersensitivity. It is estimated that up to 30% of all dogs
CC suffer from allergies or allergy-related skin disorders, and allergic
CC dermatitis is thought to affect between 3 and 15% of dogs. Common canine
CC allergens include fleas, pollens, moulds and dust, with flea allergy
CC being the most frequent. Once IgE has been released in response to
CC allergen, the IgE binds to receptors on mast cells. The IgE molecules
CC can then become cross-linked, which induces the mast cells to release
CC histamine, which leads to the manifestation of allergic symptoms. The
CC peptides of the invention correspond to epitopes of canine IgE, or
CC conservative variations thereof, that are accessible in circulating IgE
CC but not in IgE bound to mast cells. The autoantibodies produced on
CC immunisation with such peptides therefore target only circulating IgE,
CC avoiding the possibility that they may cross-link bound IgE molecules,
CC which would exacerbate an ongoing allergic response even in the absence
CC of allergen. Anti-IgE autoantibody induction results in an immune
CC response that targets the IgE-expressing B cell, which affects IgE
CC synthesis by downregulating IgE production by B cells and/or targeting
CC the IgE-producing B cell for destruction. The peptides of the invention
CC are therefore useful for the treatment or prophylaxis of allergic
CC symptoms in a dog.
SQ Sequence 11 AA;
.
Query Match 100.0%; Score 63; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GMLTWYRESK 11
1 |||||||||
1 gmltwyresk 11
DB
RESULT 2
AAY50879 standard; peptide; 11 AA.
ID AAY50879;
AC AAY50879;
AT 24-FEB-2000 (first entry)
XX
XX 8H.8 binding canine mimotope 1.
DE
XX
XX Canine; allergy; antibody 8H.8; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX
XX Synthetic.
OS
XX
XX EP957111-A2.
PN
XX
XX 17-NOV-1999.
PD
XX
XX 09-APR-1999; 99EP-0107035.
PF
XX
XX 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEXX LAB INC.
PA
XX Lawton R, Mermer B, Francoeur G;
PI
XX
XX WPI: 2000-040833/04.
DR
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT

XX Claim 10; Page 13; 30pp; English.
PS
XX
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
SQ
XX
XX Sequence 11 AA;
.
Query Match 100.0%; Score 63; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GMLTWYRESK 11
1 |||||||||
1 gmltwyresk 11
DB
RESULT 3
AAY50882 standard; peptide; 11 AA.
ID AAY50882;
AC AAY50882;
AT 24-FEB-2000 (first entry)
XX
XX
XX Antibody 8H.8 binding substituted canine mimotope 1.
DE
XX
XX Canine; allergy; antibody 8H.8; IgE; B cell; mast cell; anti-allergy;
KW epitope; prophylaxis; treatment; mimotope.
XX
XX Synthetic.
OS
XX
XX EP957111-A2.
PN
XX
XX 17-NOV-1999.
PD
XX
XX 09-APR-1999; 99EP-0107035.
PF
XX
XX 09-APR-1998; 98US-0058331.
PR 30-MAR-1999; 99US-0281760.
XX
XX (IDEXX LAB INC.
PA
XX Lawton R, Mermer B, Francoeur G;
PI
XX
XX WPI: 2000-040833/04.
DR
XX
XX Binding proteins used for treatment or prophylaxis of canine allergy -
XX
XX Example 2; Page 13; 30pp; English.
XX
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
SQ
XX
XX Sequence 11 AA;
.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:16:05 ; Search time 85.5 Seconds
(without alignments)

2.144 Million cell updates/sec

Title: US-09-281-760c-1

Perfect score: 18

Sequence: 1 LXXYR 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Immun DB seq length: 0

Post-processing: Minimum Match 0%

Database : Swissprot_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	88.9	38	1	CPRP_CANPG	P81033 cancer pagu
2	16	88.9	69	1	Y0G6_CAEEL	P34615 caenorhabdi
3	16	88.9	93	1	Y292_METJA	O57740 methanococ
4	16	88.9	99	1	SY02_HUMAN	P13500 homo sapien
5	16	88.9	99	1	SY02_NACPA	O9myr4 macaca fasc
6	16	88.9	106	1	DCMA_METTE	O08368 methanosarc
7	16	88.9	109	1	Y1R1_YEAST	P40440 saccharomyc
8	16	88.9	113	1	KV2B_HUMAN	P40165 homo sapien
9	16	88.9	191	1	YGL2_STRCO	P40182 streptomyce
10	16	88.9	195	1	CNTE_CHICK	O02011 gallus gall
11	16	88.9	199	1	TDX2_THIAC	O9hj13 thermoplas
12	16	88.9	199	1	TDX_TRYBR	O26695 trypanosoma
13	16	88.9	200	1	Y755_SYNY3	O55624 synchocyst
14	16	88.9	202	1	KAPS_YEAST	O02196 saccharomyc
15	16	88.9	207	1	CL13_HUMAN	O95833 homo sapien
16	16	88.9	211	1	KAD_TREPA	O83604 treponema p
17	16	88.9	215	1	YF52_HAEIN	P44251 haemophilus
18	16	88.9	217	1	UNG_STRAG	O9xds8 streptococ
19	16	88.9	220	1	UNG_BUCAI	P57280 buchiera ap
20	16	88.9	222	1	RS3A_METJA	P54059 methanococ
21	16	88.9	228	1	VIF_OMYVS	P16902 ovine lenti
22	16	88.9	230	1	VIF_VILV	P03403 visna lenti
23	16	88.9	230	1	VIF_VILV1	P23430 visna lenti
24	16	88.9	230	1	YD83_YEAST	O04004 saccharomyc
25	16	88.9	231	1	VIC1_AGRNH	P13459 agrobacteri
26	16	88.9	231	1	VIC1_AGRRT5	P07165 agrobacteri
27	16	88.9	231	1	VIC1_AGRRT6	P06665 agrobacteri
28	16	88.9	232	1	YFIP_ECOLI	O47319 escherichia
29	16	88.9	237	1	GSPF_PSEAE	O00517 pseudomonas
30	16	88.9	238	1	DHSB_ECOLI	P07014 escherichia
31	16	88.9	247	1	COBK_PSEDE	P21920 pseudomonas
32	16	88.9	254	1	PMY_YEAST	P07283 saccharomyc
33	16	88.9	256	1	TPSI_BRARE	O9pte6 brachydanio

ALIGNMENTS

RESULT	1	STANDARD	PRT	38 AA.
ID	CPRP_CANPG			
AC	P81033;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	CHH PRECURSOR RELATED PEPTIDE (CPRP).			
OS	Cancer pagurus (Rock crab).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eudrachyura; Cancroidea; Cancridae; Cancer.			
OX	NCBI_TaxID=6755;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Sinus gland;			
KX	MEDLINE=98025664; PubMed=9809792;			
RA	Chung J.S., Wilkinson M.C., Webster S.G.;			
RT	"Amino acid sequences of both isoforms of crustacean hyperglycemic hormone (CHH) and corresponding precursor-related peptide in Cancer pagurus."			
RL	Regul. Pept. 77:17-24(1998).			
CC	-I- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN THE ESTERALS AND TRANSPORTED TO THE SINUS GLAND WHERE IT IS STORED AND RELEASED.			
CC	Neuropeptide; Hormone.			
KW	SEQUENCE 38 AA: 3969 MW; C979C87EE31ABB90 CRC64;			
SQ				
Qy	1 LXXYR 5	88.9%; Score 16; DB 1; Length 38;		
Db	13 LASYR 17	Best Local Similarity 60.0%; Pred. No. 1.2e+02;		
		Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
RESULT	2			
ID	Y0G6_CAEEL			
AC	P34615;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	HYPOHEMIAL 7.9 KDA PROTEIN ZK112.6 IN CHROMOSOME III.			
GN	ZK112.6.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			

34	16	88.9	257	1	PMY_SCHPO	O9ntf2 schizosacch
35	16	88.9	260	1	CT12_SOLTU	P28610 solanum tub
36	16	88.9	260	1	Y4LO_RHISN	P55555 rhizobium s
37	16	88.9	261	1	TEPB_MORBO	P20666 moraxella b
38	16	88.9	262	1	GP6R_CHLMU	O9pjf7 chlamydia m
39	16	88.9	271	1	CART_MOUSE	O08331 mus musculu
40	16	88.9	271	1	CART_RAT	P47728 ratu
41	16	88.9	276	1	PYGI_SYNEL	P50039 synchococ
42	16	88.9	277	1	MSMG_STRMU	O00751 streptococ
43	16	88.9	280	1	SPEE_PYROO	O57950 pyrococcus
44	16	88.9	284	1	HUPQ_AZOCH	O43957 azotobacter
45	16	88.9	289	1	V097_MYCNU	O10893 mycobacteri
46	16	88.9	297	1	SMF_BACST	P39813 bacillus su
47	16	88.9	297	1	YNZ4_CAEEL	P45964 caenorhabdi
48	16	88.9	298	1	XERD_SALTY	P55889 salmone
49	16	88.9	308	1	Y705_DEIRA	O97wg3 deinococcus
50	16	88.9	309	1	URIC_ARATH	O04420 arabidopsis

```

RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL, NZ:
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Crofton M., Dear S., Du Z., Duthie R., Favello A., Fraser A.,
RA Fulton L., Jones M., Keshaw J., Kirszen J., Laister N., Jier M.,
RA Lavelle F., Livingston J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Riken L., Koopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sutcliffe J., Thelley-Mieg J., Thomas K., Vaudin K., Vaughan K.,
RA Watson R., Watson A., Weinstein L., Wilkinson-Sproat J.,
RA Woulman P.,
RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38(1994).
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L14324; AAA28183.1;
CC PIR: S44888; S44888.
CC WormPep: ZK112.6; CE00377.
CC Hypothetical protein.
DR SEQUENCE 69 AA; 7886 MW; 348D05DF5EB5A54A CRC64;
OY 1 LXXYR 5
OY 1 11
DB 8 LAAYR 12
Query Match 88.9%; Score 16; DB 1; Length 69;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 3
Y292.METJA STANDARD: PRT: 93 AA.
ID Y292.METJA
DC 057740;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 20-AUG-2001 (Rel. 40, Last annotation update)
DE HIPOTHETICAL PROTEIN MO292.
GN MU0292.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake O., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervase A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirnes E.F., Weissbrock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geophagen N.S.M., Weidman J.F., Fuhman J.L., Nguyen D.,
RA Utechack T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Corion M.D., Roberts R.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 277:1258-1273(1996)
CC -----
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U67484; AA98277.1;
CC DR TIGR: MO292;
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC TRANSMEM 8 28 POTENTIAL.
CC TRANSMEM 54 74 POTENTIAL.
CC FT DOMAIN 75 86 ALA-RICH.
CC SEQUENCE 93 AA; 10482 MW; B2ABCC8115AC160C CRC64;
OY 1 LXXYR 5
OY 1 11
DB 26 LAAYR 30
Query Match 88.9%; Score 16; DB 1; Length 93;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 4
SY02.HUMAN STANDARD: PRT: 99 AA.
ID SY02.HUMAN
AC P13500; O99DF3;
DI 01-JAN-1990 (Rel. 13, Created)
DI 01-JAN-1990 (Rel. 13, Last sequence update)
DI 20-AUG-2001 (Rel. 40, Last annotation update)
DE SMALL INDUCIBLE CYTOKINE A2 PRECURSOR (MONOCYTE CHEMOTACTIC
DE MCP-1) (MONOCYTE CHEMOTACTIC PROTEIN-1) (MONOCYTE CHEMOTACTIC
DE AND ACTIVATING FACTOR) (MCAF) (MONOCYTE SECRETORY PROTEIN JE) (MCL1).
DE SCY2A OR MCP1
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-89165862; PubMed-2923622;
RA Furutani T., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M.,
RA Larsen C.G., Oppenheim J.J., Matsushima K.,
RT "Cloning and sequencing of the cDNA for human monocyte chemotactic
RT and activating factor (MCAF)."
RL Biochem. Biophys. Res. Commun. 159:249-255(1989).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE-90097880; PubMed-2513477;
RA Rollins B.J., Stier P., Ernst T., Wong G.G.,
RT "The human homolog of the JE gene encodes a monocyte secretory
RT protein."
RL Mol. Cell. Biol. 9:4687-4695(1989).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE-89153605; PubMed-2465924;
RA Yoshimura T., Yoshida N., Moore S.K., Appella E., Lerman M.I.,
RA Leonard E.J.,
RT "Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA
RT cloning, expression in mitogen-stimulated blood mononuclear
RT leukocytes, and sequence similarity to mouse competence gene JE."
RL FEBS Lett. 244:487-493(1989).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE-90290466; PubMed-2357211;
RA Shyy T.-J., Li Y.-S., Koletukudy P.E.,
RT "Structure of human monocyte chemotactic protein gene and its
RT regulation by TPA."
RL Biochem. Biophys. Res. Commun. 169:346-351(1990).
RN [5]

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:11:15 ; Search time 102.84 Seconds
(without alignments)
3.704 Million cell updates/sec

Title: US-09-281-760C-1
Perfect score: 18
Sequence: 1 LXXR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	88.9	69	2	S44888
2	16	88.9	74	2	T13344
3	16	88.9	92	2	T09146
4	16	88.9	93	2	I47624
5	16	88.9	93	2	E64336
6	16	88.9	99	2	A60299
7	16	88.9	101	2	T37064
8	16	88.9	101	2	D82808
9	16	88.9	105	2	E69058
10	16	88.9	105	2	H72533
11	16	88.9	106	2	A48868
12	16	88.9	109	2	S50356
13	16	88.9	109	2	B72615
14	16	88.9	113	1	K2HUF9
15	16	88.9	114	2	S22559
16	16	88.9	117	2	T41216
17	16	88.9	130	1	A69894
18	16	88.9	130	2	A35946
19	16	88.9	130	2	T44809
20	16	88.9	132	2	F70650
21	16	88.9	140	2	H75426
22	16	88.9	146	2	E75289
23	16	88.9	148	2	C71263
24	16	88.9	149	2	H70638
25	16	88.9	151	2	H75298
26	16	88.9	152	2	B72690
27	16	88.9	156	2	D84499
28	16	88.9	161	2	T35369
29	16	88.9	161	2	G83914

30	16	88.9	165	2	T01421	pistil extensin-11
31	16	88.9	166	2	B83700	hypothetical prote
32	16	88.9	168	2	E83437	hypothetical prote
33	16	88.9	170	2	S76417	hypothetical prote
34	16	88.9	175	2	T15067	hypothetical prote
35	16	88.9	176	2	G84214	hypothetical prote
36	16	88.9	181	2	C84233	hypothetical prote
37	16	88.9	190	2	S41476	calretinin - mouse
38	16	88.9	191	2	T35508	hypothetical prote
39	16	88.9	195	2	JH0680	ciliary neurotroph
40	16	88.9	200	2	S76284	hypothetical prote
41	16	88.9	202	1	S17244	adenylylsulfate ki
42	16	88.9	206	2	T22345	hypothetical prote
43	16	88.9	207	2	B27626	hypothetical prote
44	16	88.9	210	2	S27489	probable lipoprote
45	16	88.9	210	2	T22344	hypothetical prote
46	16	88.9	211	2	D71306	probable adenylate
47	16	88.9	212	2	H83547	probable acyl carr
48	16	88.9	215	2	I64035	hypothetical prote
49	16	88.9	219	2	B81908	probable uracil-DN
50	16	88.9	219	2	H81107	uracil-DNA glycosy

ALIGNMENTS

RESULT 1
S44888
ZK112.6 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C:Accession: S44888
R:Du, Z.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZK112.
A:Reference number: S44616
A:Accession: S44888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-69 <DUZ>
A:Cross-References: EMBL:L14324; NID:g289740; PID:g289743
C:Genetics:
A:Introns: 20/3

Query Match 88.9%; Score 16; DB 2; Length 69;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXR 5
DB 8 LAAYR 12

RESULT 2
T13344
hypothetical protein 55 - Streptococcus phage phi-01205
C:Species: Streptococcus phage phi-01205
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Sep-1999
C:Accession: T13344
R:Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.
Microbiology 143, 3417-3429, 1997
A:Title: Sequence analysis and characterization of phi 01205, a temperate bacteriophage
A:Reference number: 217654; MUID:98048466
A:Accession: T13344
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-74 <STA>
A:Cross-References: EMBL:U88974; NID:g2444080; PID:g2444135; PIDN:AAC79571.1
A:Experimental source: host Streptococcus thermophilus strain CNR21205

Query Match 88.9%; Score 16; DB 2; Length 74;

Best Local Similarity 60.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXR 5
1 1 1
59 LSAYR 63

RESULT 3

T09146
late-embryogenesis protein EMB11 - white spruce
C:Species: Picea glauca (white spruce)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T09146
R: Dong, J.Z.; Dunstan, D.I.
Submitted to the EMBL Data Library, June 1996
A: Description: Gene expression during somatic embryogenesis.
A: Reference number: Z16588
A: Accession: T09146
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-92 <DON>
A: Cross-references: EMBL: L47628; NID: G1350491; PID: G1350492
C: Genetics:

Query Match 88.9%; Score 16; DB 2; Length 92;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXR 5
1 1 1
6 LSAYR 10

RESULT 4

I47624
Ig heavy chain V-VIII region - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
C:Accession: I47624
R: Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A: Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A: Reference number: A47624; MUID: 90237760
A: Accession: I47624
A: Status: preliminary; not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-93 <HA1>
C: Superfamily: Immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotrimer; immunoglobulin

Query Match 88.9%; Score 16; DB 2; Length 93;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXR 5
1 1 1
47 LSAYR 51

RESULT 5

E64336
conserved hypothetical protein M30292 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: E64336
R: Bully, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
J. Reich, C.F.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodok, A.;
Tison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996

A: Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Noese
A: Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A: Reference number: A64300; MUID: 9637799
A: Accession: E64336
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-93 <BUL>
A: Cross-references: GB: U67484; GB: L77117; NID: G1591009; PID: AAB98277.1; PID: G1591014
C: Genetics:
A: Map position: REV275415-275134
A: Start codon: TTG
C: Superfamily: Methanococcus jannaschii conserved hypothetical protein M30292

Query Match 88.9%; Score 16; DB 2; Length 93;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXR 5
1 1 1
26 LSAYR 30

RESULT 6

A60299
monocyte chemoattractant protein 1 precursor - human.
N: Alternate names: GDCF-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1;
N: Contains: glioma-derived chemotactic factor 2 (GDCF-2)
C: Species: Homo sapiens (man)
C: Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 16-Jul-1999
C: Accession: A33474; A33476; S03339; I51841; A60299; A32300; A32396; A34561; I57488;
R: Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 169, 346-351, 1990
A: Title: Structure of human monocyte chemotactic protein gene and its regulation by T
A: Reference number: A33474; MUID: 90290466
A: Accession: A33474
A: Molecule type: DNA
A: Residues: 1-99 <SHY>
A: Cross-references: GB: M37719; NID: G187447; PID: AAA18102.1; PID: G487124
R: Rollins, B.J.; Stier, P.; Ernst, T.; Wong, G.G.
Mol. Cell. Biol. 9, 4687-4695, 1989
A: Title: The human homology of the JE gene encodes a monocyte secretory protein.
A: Reference number: A33476; MUID: 90097880
A: Accession: A33476
A: Molecule type: mRNA
A: Residues: 1-99 <ROU>
A: Cross-references: GB: M30816; GB: M31625; GB: M31626; NID: G188701; PID: AAA6330.1; PI
R: Yoshimura, T.; Yoshida, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J.
Proc. Natl. Acad. Sci. USA 86, 1989
A: Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning,
A: Reference number: S03339; MUID: 89153605
A: Accession: S03339
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 1-99 <ROS>
A: Cross-references: GB: X14768; NID: G34513; PID: CAA32876.1; PID: G34514
A: Experimental source: glioma cell line U-105SK
R: Yoshimura, T.; Leonard, E.J.
Adv. Exp. Med. Biol. 305, 47-56, 1991
A: Title: Human monocyte chemoattractant protein-1 (MCP-1).
A: Reference number: I51841; MUID: 92095166
A: Accession: I51841
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-99 <O2>
A: Cross-references: GB: S71513; NID: G240867; PID: AAB20651.1; PID: G240868
R: Botatzaki, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.
Int. J. Cancer 45, 795-797, 1990
A: Title: A chemotactant expressed in human sarcoma cells (tumor-derived chemotactant-1/MCAF).
A: Reference number: A60299; MUID: 90216082
A: Accession: A60299

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:14:20 ; Search time 191.29 Seconds
(without alignments)
3.823 Million cell updates/sec

Title: US-09-281-760c-1
Perfect score: 18
Sequence: 1 LXXYR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP TREMBL.17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	88.9	44	6 Q9BG83	Q9BG83 pongo pygma
2	16	88.9	59	6 Q97749	Q97749 bos taurus
3	16	88.9	74	2 Q34086	Q34086 streptococ
4	16	88.9	74	9 Q21986	Q21986 streptococ
5	16	88.9	78	1 Q9V2Y7	Q9V2Y7 methanobact
6	16	88.9	84	5 P91813	P91813 toxocara ca
7	16	88.9	90	2 Q50475	Q50475 proteus vul
8	16	88.9	91	12 Q72831	Q72831 human immun
9	16	88.9	92	10 Q40840	Q40840 picea glauc
10	16	88.9	94	9 Q9MC42	Q9MC42 bacterioph
11	16	88.9	97	6 Q77661	Q77661 papio anubi
12	16	88.9	101	2 Q9S1Z2	Q9S1Z2 streptomyc
13	16	88.9	101	2 Q9PG85	Q9PG85 xylella fas
14	16	88.9	102	9 Q9AYW1	Q9AYW1 lactococcus
15	16	88.9	102	13 Q9DDQ7	Q9DDQ7 decapterus
16	16	88.9	102	13 Q9DDQ5	Q9DDQ5 decapterus
17	16	88.9	102	13 Q9DDQ4	Q9DDQ4 decapterus
18	16	88.9	102	13 Q9DDQ3	Q9DDQ3 decapterus
19	16	88.9	102	13 Q9DDQ1	Q9DDQ1 decapterus

20	16	88.9	102	13 Q9DDP0	Q9DDP0 decapterus
21	16	88.9	102	13 Q9DDP9	Q9DDP9 decapterus
22	16	88.9	102	13 Q9DD71	Q9DD71 decapterus
23	16	88.9	103	2 Q9KW07	Q9KW07 pseudomonas
24	16	88.9	105	1 Q27488	Q27488 methanobact
25	16	88.9	105	1 Q9Y9P4	Q9Y9P4 aeropyrum p
26	16	88.9	109	1 Q9YC72	Q9YC72 aeropyrum p
27	16	88.9	110	12 Q99GX6	Q99GX6 helicocarp
28	16	88.9	111	5 Q9GXZ4	Q9GXZ4 leishmania
29	16	88.9	112	2 Q9AJZ8	Q9AJZ8 streptomyc
30	16	88.9	117	3 Q9Y7P7	Q9Y7P7 schizosacch
31	16	88.9	118	2 Q9LSM8	Q9LSM8 salmonella
32	16	88.9	121	8 Q9TAP8	Q9TAP8 heterophyes
33	16	88.9	126	4 Q14956	Q14956 homo sapien
34	16	88.9	128	11 Q9R2C0	Q9R2C0 ratius norv
35	16	88.9	130	1 Q9HHI0	Q9HHI0 halobacteri
36	16	88.9	130	2 Q34506	Q34506 bacillus su
37	16	88.9	130	2 Q9R9I8	Q9R9I8 bacillus su
38	16	88.9	130	2 Q9L7W8	Q9L7W8 bacillus su
39	16	88.9	130	10 Q9M4G0	Q9M4G0 arabidopsis
40	16	88.9	132	2 P95089	P95089 mycobacteri
41	16	88.9	135	12 Q68190	Q68190 hepatitis c
42	16	88.9	139	2 Q9RDQ0	Q9RDQ0 streptomyc
43	16	88.9	140	2 Q9RV53	Q9RV53 deinococcus
44	16	88.9	141	2 Q9F8M4	Q9F8M4 carboxydoth
45	16	88.9	143	10 Q9XEV8	Q9XEV8 chlamydomon
46	16	88.9	144	2 Q9CB66	Q9CB66 mycobacteri
47	16	88.9	144	2 Q99YG4	Q99YG4 streptococ
48	16	88.9	146	2 Q9RS06	Q9RS06 deinococcus
49	16	88.9	148	2 Q83913	Q83913 treponema p
50	16	88.9	149	2 P95258	P95258 mycobacteri

ALIGNMENTS

RESULT 1
ID Q9BG83 PRELIMINARY: PRT: 44 AA.
AC Q9BG83;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MONOCYTE CHEMOTACTIC PROTEIN 1 (FRAGMENT).
GN MCP1.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxId=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Ayl T.C., Chew X.L.A., Yap P.H.E.;
RT *Comparison between human and primate genomes.*;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF324469; AAK13442.1; .
FT NON_TER 1 44
FT NON_TER 1 44
SQ SEQUENCE 44 AA: 4830 MW: 1DE3C10BB83CDI90 CRC64;

Query Match 88.9%; Score 16; DB 6; Length 44;
Best Local Similarity 60.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;

OY 1 LXXYR 5
DB 40 LASTYR 44
RESULT 2
ID Q97749 PRELIMINARY: PRT: 59 AA.
AC Q97749;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE BOVINE PROTHROMBIN MRNA, PARTIAL CDS (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86077733; PubMed=3000440;
 RA Irtin D.M., Ahern K.G., Pearson G.D.N., Macgillivray R.T.A.;
 RT "Characterization of the bovine prothrombin gene."
 RL Biochemistry 24:6854-6861(1985).
 DR EMBL: M12045; AAA30780.1; -.
 FT NON_TER
 FT NON_TER
 Q SEQUENCE 59 AA; 6641 MW; 5570708FA94A74A CRC64;

Query Match 88.9%; Score 16; DB 6; Length 59;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LXXYR 5
 Db 17 LYSR 21

RESULT 3
 O34086 PRELIMINARY; PRT; 74 AA.
 AC O34086;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE ORE55.
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CMR21205;
 RA Stanley E., Fitzgerald G.F., Le Marrec C., Fayard B., van Sinderen D.;
 RT "Sequence analysis and characterization of phi O1205, a temperate
 bacteriophage infecting Streptococcus thermophilus CMR21205."
 RL Microbiology 143:0-0(0).
 DR EMBL: U86974; AAC79571.1; -.
 SQ SEQUENCE 74 AA; 8609 MW; 141FE219D50BBD1 CRC64;

Query Match 88.9%; Score 16; DB 2; Length 74;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LXXYR 5
 Db 59 LSAVR 63

RESULT 4
 O21986 PRELIMINARY; PRT; 74 AA.
 AC O21986;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 12, Last annotation update)
 DE ORF74A PROTEIN.
 OS Streptococcus thermophilus bacteriophage Sf121.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.

OC NCBI_TaxID=64186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96204576; PubMed=8623559;
 RA Bruttin A., Brussov H.;
 RT "Site-specific spontaneous deletions in three genome regions of a
 temperate Streptococcus thermophilus phage."
 RL Virology 219:96-104(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97344856; PubMed=9201223;
 RA Bruttin A., Desiere F., Lucchini S., Foley S., Brussov H.;
 RT "Characterization of the lysogeny DNA module from the temperate
 Streptococcus thermophilus bacteriophage phi Sf121."
 RL Virology 233:136-148(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98160788; PubMed=9499809;
 RA Desiere F., Lucchini S., Brussov H.;
 RT "Evolution of Streptococcus thermophilus bacteriophage genomes by
 modular exchanges followed by point mutations and small deletions and
 insertions."
 RL Virology 241:345-356(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Desiere F., Lucchini S., Bruttin A., Brussov H.;
 RT "Streptococcus thermophilus bacteriophage Sf121 complete genome."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X95646; CAA64946.1; -.
 DR EMBL: AF15103; AAD44092.1; -.
 SQ SEQUENCE 74 AA; 8592 MW; 12D73E275B95E3F CRC64;

Query Match 88.9%; Score 16; DB 9; Length 74;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LXXYR 5
 Db 59 LSAVR 63

RESULT 5
 O9V2Y7 PRELIMINARY; PRT; 78 AA.
 AC O9V2Y7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE TRANSMEMBRANE PROTEIN 8.3 KDA.
 GN EHD.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacter.
 OC NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=MARBURG;
 RA Tersteegen A., Hedderich R.;
 RT "Methanobacterium thermoautotrophicum encodes two multisubunit
 membrane-bound [Nife] hydrogenases. Transcription of the operons and
 sequence analysis of the deduced proteins."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ243656; CAB52781.1; -.
 KW Transmembrane.
 SQ SEQUENCE 78 AA; 8285 MW; 1CEDDF8DC27F63D7 CRC64;

Query Match 88.9%; Score 16; DB 1; Length 78;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LXXYR 5

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:11:10 ; Search time 158.02 Seconds
(without alignments)
2.344 Million cell updates/sec

Title: US-09-281-760c-1
Perfect score: 18
Sequence: 1 LXXVR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

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22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	88.9	7	20	AAV34076
2	16	88.9	7	20	AAV34080
3	16	88.9	7	20	AAV34084
4	16	88.9	10	22	AAV34084
5	16	88.9	11	12	AAV34084
6	16	88.9	11	15	AAV34084
7	16	88.9	11	15	AAV34084
8	16	88.9	11	15	AAV34084
9	16	88.9	23	21	AAV34084
10	16	88.9	23	22	AAV34084
11	16	88.9	23	22	AAV34084

12	16	88.9	23	22	AAV72693
13	16	88.9	24	22	AAV72682
14	16	88.9	26	22	AAV72683
15	16	88.9	29	20	AAV12972
16	16	88.9	38	15	AAV58398
17	16	88.9	49	22	AAV74890
18	16	88.9	53	20	AAV45304
19	16	88.9	55	20	AAV48467
20	16	88.9	59	22	AAV17762
21	16	88.9	59	22	AAV30271
22	16	88.9	59	22	AAV05416
23	16	88.9	60	22	AAV74441
24	16	88.9	60	21	AAV58811
25	16	88.9	66	18	AAV13598
26	16	88.9	66	21	AAV55104
27	16	88.9	67	18	AAV13599
28	16	88.9	68	18	AAV13597
29	16	88.9	68	20	AAV95035
30	16	88.9	68	20	AAV95036
31	16	88.9	68	20	AAV95037
32	16	88.9	69	16	AAV87678
33	16	88.9	69	18	AAV13596
34	16	88.9	76	10	AAV90292
35	16	88.9	76	13	AAV28660
36	16	88.9	76	15	AAV53398
37	16	88.9	76	16	AAV87680
38	16	88.9	76	16	AAV87676
39	16	88.9	76	17	AAV87677
40	16	88.9	76	17	AAV09374
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42	16	88.9	76	19	AAV40175
43	16	88.9	76	21	AAV12818
44	16	88.9	76	21	AAV69030
45	16	88.9	77	16	AAV86859
46	16	88.9	77	20	AAV14222
47	16	88.9	78	21	AAV10256
48	16	88.9	79	22	AAV24442
49	16	88.9	90	21	AAV01263
50	16	88.9	96	15	AAV51942

ALIGNMENTS

RESULT 1	
AAV34076	AAV34076 standard; peptide; 7 AA.
ID	AAV34076;
AC	AAV34076;
XX	
XX	23-NOV-1999 (first entry)
DE	Bacteroides 100 kDa antigen peptide fragment.
XX	
XX	ulcerative colitis; histone; H1-like antigen; porin antigen;
KW	Bacteroides antigen; inflammatory bowel disease; IBD; PANCA;
KW	perinuclear anti-neutrophil cytoplasmic antibody; diagnosis.
XX	
OS	Bacteroides cacciae.
XX	
PN	WO945955-A1.
PD	16-SEP-1999.
XX	
PE	12-MAR-1999; 99MO-US05492.
XX	
PR	12-MAR-1998; 98US-0041889.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Braun J, Cohavy O;
XX	
DR	WPI, 1999-551215/46.

Human monocytic che
Human monocytic che
Human monocytic che
Protein sequence o
TSAR binding domai
Human colon cancer
Human secreted pro
Human breast tumor
Peptide #4196 enco
Peptide #4308 enco
Peptide #4098 enco
Human colon cancer
Breast and ovarian
Monocyte chemoattr
Arbidiopsis thalia
Monocyte chemoattr
Monocyte chemoattr
MCP-1 analogue [V9
MCP-1 analogue [V9
des(2-8) MCP-1. H
Monocyte chemoattr
Peptide from human
MCP. Synthetic.
Sense MCP-1. Mamm
Monocyte chemoattr
(24-Arg) MCP-1. H
(3-Ala) MCP-1. Ho
Monocyte chemoattr
Mature human monoc
Macrophage chemoat
Human glioma cell
Amino acid sequenc
Mature MCP-1. Hom
Chemokine hMCP1.
Human adult retina
Human EST encoded
Human secreted pro
Sequence of M. pul

XX Use of histone H1, porin or Bacteroides antigens as targets for the
 PT diagnosis, prevention and treatment of ulcerative colitis.
 XX
 XX
 PS Example 6; Page 78; 134pp; English.

XX The invention provides a method for the diagnosis, prevention and
 CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a
 CC porin antigen or a Bacteroides antigen as a target antigen. The novel
 CC method of diagnosing UC in a subject suspected of having inflammatory
 CC bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
 CC (2) contacting the sample with a histone H1-like antigen, or perinuclear
 CC anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form
 CC a complex of the histone H1-like antigen, or the PANCA-reactive
 CC fragment, and antibody to the histone H1-like antigen; and (3) detecting
 CC the presence or absence of the complex; where the presence of the
 CC complex indicates that the subject has UC. The PANCA-reactive histone
 CC H1-like antigen, porin antigen and Bacteroides antigen are useful in the
 CC diagnosis, prevention and treatment of UC. The methods can also be used
 CC for identifying agents useful for treating UC. Sequences AAY34072-87
 CC represent peptides derived from the B. caccae 100 kda antigen (a
 CC microbial PANCA-reactive protein).

CC Sequence 7 AA:

Query Match 88.9%; Score 16; DB 20; Length 7;
 Best Local Similarity 60.0%; Pred. No. 4.3e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXYR 5
 | |
 Db 3 lasyr 7

RESULT 2

AAAY34080 standard; peptide; 7 AA.

AC AAY34080;

DT 23-NOV-1999 (first entry)

DE Bacteroides 100 kda antigen peptide fragment.

XX Ulcerative colitis; histone; H1-like antigen; porin antigen;
 KM Bacteroides antigen; inflammatory bowel disease; IBD; PANCA;
 KM perinuclear anti-neutrophil cytoplasmic antibody; diagnosis.

XX Bacteroides caccae.

OS WO945955-A1.

PM 16-SEP-1999.

XX 12-MAR-1999; 99WO-0505492.

XX 12-MAR-1998; 98US-0041889.

XX (REGC) UNIV CALIFORNIA.

PA Braun J, Cohavy O;

PI WPI; 1999-551215/46.

XX Use of histone H1, porin or Bacteroides antigens as targets for the
 PT diagnosis, prevention and treatment of ulcerative colitis.
 XX
 PS Example 6; Page 78; 134pp; English.

XX The invention provides a method for the diagnosis, prevention and
 CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a
 CC porin antigen or a Bacteroides antigen as a target antigen. The novel

CC method of diagnosing UC in a subject suspected of having inflammatory
 CC bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
 CC (2) contacting the sample with a histone H1-like antigen, or perinuclear
 CC anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form
 CC a complex of the histone H1-like antigen, or the PANCA-reactive
 CC fragment, and antibody to the histone H1-like antigen; and (3) detecting
 CC the presence or absence of the complex; where the presence of the
 CC complex indicates that the subject has UC. The PANCA-reactive histone
 CC H1-like antigen, porin antigen and Bacteroides antigen are useful in the
 CC diagnosis, prevention and treatment of UC. The methods can also be used
 CC for identifying agents useful for treating UC. Sequences AAY34072-87
 CC represent peptides derived from the B. caccae 100 kda antigen (a
 CC microbial PANCA-reactive protein).

SO Sequence 7 AA:

Query Match 88.9%; Score 16; DB 20; Length 7;
 Best Local Similarity 60.0%; Pred. No. 4.3e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXYR 5
 | |
 Db 3 lasyr 7

RESULT 3

AAAY34084 standard; peptide; 7 AA.

AC AAY34084;

DT 23-NOV-1999 (first entry)

DE Bacteroides 100 kda antigen peptide fragment.

XX Ulcerative colitis; histone; H1-like antigen; porin antigen;
 KM Bacteroides antigen; inflammatory bowel disease; IBD; PANCA;
 KM perinuclear anti-neutrophil cytoplasmic antibody; diagnosis.

XX Bacteroides caccae.

OS WO945955-A1.

PM 16-SEP-1999.

XX 12-MAR-1999; 99WO-0505492.

XX 12-MAR-1998; 98US-0041889.

XX (REGC) UNIV CALIFORNIA.

PA Braun J, Cohavy O;

PI WPI; 1999-551215/46.

XX Use of histone H1, porin or Bacteroides antigens as targets for the
 PT diagnosis, prevention and treatment of ulcerative colitis.
 XX
 PS Example 6; Page 78; 134pp; English.

XX The invention provides a method for the diagnosis, prevention and
 CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a
 CC porin antigen or a Bacteroides antigen as a target antigen. The novel
 CC method of diagnosing UC in a subject suspected of having inflammatory
 CC bowel disease (IBD) comprises: (1) obtaining a sample from the subject;
 CC (2) contacting the sample with a histone H1-like antigen, or perinuclear
 CC anti-neutrophil cytoplasmic antibody (PANCA)-reactive fragment, to form
 CC a complex of the histone H1-like antigen, or the PANCA-reactive
 CC fragment, and antibody to the histone H1-like antigen; and (3) detecting
 CC the presence or absence of the complex; where the presence of the
 CC complex indicates that the subject has UC. The PANCA-reactive histone
 CC H1-like antigen, porin antigen and Bacteroides antigen are useful in the

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:11:15 ; Search time 94.43 Seconds

(without alignments)
1.192 Million cell updates/sec

Title: US-09-281-760C-1

Perfect score: 18

Sequence: 1 LXXR 5

Scoring table: BLOSUM62

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	16	88.9	38	1	US-08-189-331-56
5	16	88.9	38	2	US-08-471-939-56
6	16	88.9	38	2	US-08-471-800-56
7	16	88.9	38	2	US-08-471-068-56
8	16	88.9	69	4	US-08-855-526B-44
9	16	88.9	76	1	US-07-956-862A-1
10	16	88.9	76	1	US-08-250-958-1
11	16	88.9	76	1	US-08-235-659-1
12	16	88.9	76	2	US-08-716-188-2
13	16	88.9	76	2	US-08-615-232A-5
14	16	88.9	76	3	US-08-470-333-5
15	16	88.9	78	1	US-08-330-163-12
16	16	88.9	78	1	US-08-482-111-12
17	16	88.9	78	5	PCT-US95-00605-1
18	16	88.9	96	5	PCT-US93-08744-4
19	16	88.9	99	1	US-08-127-499A-35
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31	16	88.9	99	3	US-09-044-855A-5	Sequence 5, Appl
32	16	88.9	99	4	US-08-679-493A-152	Sequence 152, App
33	16	88.9	99	5	PCT-US96-10087-5	Sequence 5, Appl
34	16	88.9	99	6	5212073-2	Patent No. 5212073
35	16	88.9	121	1	US-08-420-235B-23	Sequence 23, Appl
36	16	88.9	121	1	US-08-793-624-23	Sequence 23, Appl
37	16	88.9	121	5	PCT-US95-10194-23	Sequence 23, Appl
38	16	88.9	191	1	US-08-159-784-3	Sequence 3, Appl
39	16	88.9	195	1	US-07-959-284-5	Sequence 5, Appl
40	16	88.9	195	2	US-08-308-735A-5	Sequence 5, Appl
41	16	88.9	195	5	PCT-US92-08258-2	Sequence 2, Appl
42	16	88.9	195	5	PCT-US93-08648A-5	Sequence 2, Appl
43	16	88.9	195	5	PCT-US93-08648-5	Sequence 5, Appl
44	16	88.9	249	4	US-08-591-468-2	Sequence 2, Appl
45	16	88.9	249	5	PCT-US94-06430-2	Sequence 2, Appl
46	16	88.9	294	4	US-09-242-948-2	Sequence 2, Appl
47	16	88.9	312	4	US-09-242-948-4	Sequence 4, Appl
48	16	88.9	317	2	US-08-767-096-2	Sequence 2, Appl
49	16	88.9	317	4	US-09-480-203-2	Sequence 2, Appl
50	16	88.9	334	2	US-08-665-647-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
5177060-30
Patent No. 5177060
APPLICANT: WEI, EDWARD T.
TITLE OF INVENTION: ANTI-INFLAMMATORY PEPTIDES AND TREATMENT
TO INHIBIT VASCULAR LEAKAGE IN INJURED TISSUES
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,578
FILING DATE: 09-JAN-1990
SEQ ID NO:30:
LENGTH: 11
5177060-30

Query Match 88.9%; Score 16; Length 11;
Best Local Similarity 60.0%; Pred. No. 77;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXR 5
Db 1 LATYR 5

RESULT 2
US-08-176-500-56
Sequence 56, Application US/08176500
Patent No. 5498538
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennale & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/176,500
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/013,416
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MISTOCK, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 790-9090
;; TELEFAX: 212 869-8864/9741
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-176-500-56

Query Match 88.9%; Score 16; DB 1; Length 38;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXYR 5
DB 26 LYSYR 30

;; RESULT 3
;; US-08-471-052A-56
;; Sequence 56, Application US/08471052A
;; Patent No. 5625033
;; GENERAL INFORMATION:
;; APPLICANT: Kay, B. K.
;; APPLICANT: Fowlkes, D. M.
;; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
;; NUMBER OF SEQUENCES: 166
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/471,052A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MISTOCK, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-179
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 790-9090
;; TELEFAX: 212 869-8864/9741
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown

;; MOLECULE TYPE: peptide
;; US-08-471-052A-56

Query Match 88.9%; Score 16; DB 1; Length 38;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXYR 5
DB 26 LYSYR 30

;; RESULT 4
;; US-08-189-331-56
;; Sequence 56, Application US/08189331
;; Patent No. 5747334
;; GENERAL INFORMATION:
;; APPLICANT: Kay, B. K.
;; APPLICANT: Fowlkes, D. M.
;; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
;; NUMBER OF SEQUENCES: 186
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/189,331
;; FILING DATE: Concurrently herewith
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MISTOCK, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-155
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212 790-9090
;; TELEFAX: 212 869-8864/9741
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 38 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
;; US-08-189-331-56

Query Match 88.9%; Score 16; DB 1; Length 38;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXYR 5
DB 26 LYSYR 30

;; RESULT 5
;; US-08-471-939-56
;; Sequence 56, Application US/08471939
;; Patent No. 5844076
;; GENERAL INFORMATION:
;; APPLICANT: Kay, B. K.
;; APPLICANT: Fowlkes, D. M.
;; TITLE OF INVENTION: Totally Synthetic Affinity Reagents

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:17:53 ; Search time 102.84 Seconds
(without alignments)
3.704 Million cell updates/sec

Title: US-09-281-760C-2

Perfect score: 18

Sequence: 1 YRXXL 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: PIR_68:*
2: PIR:*
3: PIR:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	88.9	56	2	T39209
2	16	88.9	68	2	S22327
3	16	88.9	75	2	H59096
4	16	88.9	81	2	S01059
5	16	88.9	83	2	A49355
6	16	88.9	83	2	T14380
7	16	88.9	101	4	S59321
8	16	88.9	102	2	C96595
9	16	88.9	102	2	A84266
10	16	88.9	112	2	C75298
11	16	88.9	114	2	F85843
12	16	88.9	114	2	B85692
13	16	88.9	114	2	B85681
14	16	88.9	114	2	B85630
15	16	88.9	118	2	T05812
16	16	88.9	119	1	MSPE
17	16	88.9	124	2	B48983
18	16	88.9	130	2	H69699
19	16	88.9	130	2	T47309
20	16	88.9	131	2	H69062
21	16	88.9	131	2	A84491
22	16	88.9	132	2	S77266
23	16	88.9	133	1	S24315
24	16	88.9	139	2	T03486
25	16	88.9	151	2	S69472
26	16	88.9	152	2	T44544
27	16	88.9	156	2	E84230
28	16	88.9	159	2	E83346
29	16	88.9	160	2	T04633

30	16	88.9	175	2	D86471	hypothetical prote
31	16	88.9	176	2	T47361	hypothetical prote
32	16	88.9	182	2	T49540	hypothetical prote
33	16	88.9	184	2	A83722	hypothetical prote
34	16	88.9	185	2	A28677	aminoacylcoside N6'
35	16	88.9	188	2	D75499	probable acetyltra
36	16	88.9	189	2	T05905	ids-4 protein - ba
37	16	88.9	189	2	D83008	outer membrane lip
38	16	88.9	189	2	C71427	hypothetical prote
39	16	88.9	190	2	T28093	hypothetical prote
40	16	88.9	194	2	T11928	ribosomal protein
41	16	88.9	195	2	A75295	conserved hypotet
42	16	88.9	197	2	C82619	HeII protein XFI93
43	16	88.9	198	2	J01052	repressor protein
44	16	88.9	199	2	D82865	conjugal transfer
45	16	88.9	200	2	D83116	50S ribosomal prot
46	16	88.9	201	2	F82604	conjugal transfer
47	16	88.9	202	2	G71295	conserved hypotet
48	16	88.9	203	2	T18653	hypothetical prote
49	16	88.9	206	2	E75345	peptide methionine
50	16	88.9	208	2	T30859	fertility inhibiti

ALIGNMENTS

RESULT 1
T39209
very hypothetical protein SPAC9E9.17c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39209
R:McDougal, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21836
A:Accession: T39209
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-56 <MCD>
A:Cross-references: EMBL:Z99262; PIDN:CAB58229.1; GSPDB:GN00066; SPDB:SPAC9E9.17c
A:Experimental source: strain 972h-; cosmid c9E9
C:Genetics:
A:Gene: SPDB:SPAC9E9.17c
A:Map position: 1
A:introns: 27/2

Query Match 88.9%; Score 16; DB 2; Length 56;
Best local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRXXL 5
DB 37 YRRTL 41

RESULT 2
S22327
gene C protein - phage alpha-3
C:Species: phage alpha-3
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 20-Sep-1999
C:Accession: S22327
R:Kodaira, K.I.; Nakano, K.; Okada, S.; Taketo, A.
Biochim. Biophys. Acta 1130, 277-286, 1992
A:title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelation
A:Reference number: S22324; MUID:92223109
A:Accession: S22327
A:Molecule type: DNA
A:Residues: 1-68 <KOD>
A:Cross-references: EMBL:X60322; NID:g14775; PIDN:CAA42877.1; PID:g14779
C:Genetics:
A:Gene: C
C:superfamily: phage phi-X174 gene C protein

Query Match 88.9%; Score 16; DB 2; Length 68;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
|||
DB 11 YRATL 15

RESULT 3
H59096
hypothetical protein PX01-48 - Bacillus anthracis virulence plasmid PX01
C:Species: Bacillus anthracis
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C:Accession: H59096
R:Oklnaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J.; Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of PX01, the large Bacillus anthracis plasmid harbored
by B. anthracis
A:Reference number: A59091; MUID:99445483
A:Accession: H59096
A:Status: preliminary
A:Residues: 1-75 <OK>
A:Molecule type: DNA
A:Cross-references: GB:AF065404; NID:g4894216; PIDN:MD32352.1; PID:g4894264
C:Experimental source: strain Sterne
C:Genetics:
A:Gene: PX01-48
A:genome: plasmid

Query Match 88.9%; Score 16; DB 2; Length 75;
Best Local Similarity 60.0%; Pred. No. 5.4e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
|||
DB 70 YRRTL 74

RESULT 4
S01059
hypothetical protein 2 - rice
C:Species: Oryza sativa (rice)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Jul-2000
C:Accession: S01059
R:Kikuchi, S.; Takaiwa, F.; Oono, K.
Mol. Gen. Genet. 210, 373-380, 1987
A:Title: Variable copy number DNA sequences in rice.
A:Reference number: S01057; MUID:88121710
A:Accession: S01059
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-81 <KIK>
A:Cross-references: EMBL:X06611; NID:g20380; PIDN:CAA9826.1; PID:g20383

Query Match 88.9%; Score 16; DB 2; Length 81;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
|||
DB 3 YRSSL 7

RESULT 5
A49355
cytochrome-c oxidase (EC 1.9.3.1) chain VIIA precursor, isoform L - bovine
M:Alternate names: cytochrome-c oxidase chain VIIA, hepatic
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 11-Jun-1999

C:Accession: A49355; B41034; S07891; C29968
R:Seelan, R.S.; Grossman, L.I.
Genomics 18, 527-536, 1993
A:Title: Structural organization and evolution of the liver isoform gene for bovine c
A:Reference number: A49355; MUID:94140349
A:Accession: A49355
A:Molecule type: DNA
A:Residues: 1-83 <SE3>
A:Cross-references: GB:I09603; NID:g451884; PIDN:AAA18218.1; PID:g488158
R:Seelan, R.S.; Grossman, L.I.
J. Biol. Chem. 266, 19752-19757, 1991
A:Title: Cytochrome c oxidase subunit VIIA isoforms. Characterization and expression
A:Reference number: S18187; MUID:92011781
A:Accession: B41034
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-83 <SE3>

A:Note: this corrects the sequence reported with accession number S07891
R:Seelan, R.S.; Schenker, D.; Lomax, M.I.; Grossman, L.I.
Nucleic Acids Res. 17, 6410, 1989
A:Title: Nucleotide sequence of a cDNA for bovine cytochrome c oxidase subunit VIIA.
A:Reference number: S07891; MUID:8936688
A:Accession: S07891
A:Molecule type: mRNA
A:Residues: 1-52; R, 54-83 <SE2>
A:Cross-references: EMBL:X15235; NID:g273; PIDN:CAA3313.1; PID:g274
R:Yanamura, W.; Zhang, Y.Z.; Takamiya, S.; Capaldi, R.A.
Biochemistry 27, 4909-4914, 1988
A:Title: Tissue-specific differences between heart and liver cytochrome c oxidase.
A:Reference number: A90531; MUID:89000697
A:Accession: C29968
A:Molecule type: Protein
A:Residues: 24-51, 'N', 54-56, 'V', 58, 'W', 60 <YAN>
A:Experimental source: liver
C:Genetics:

A:Gene: COX7AL
A:Introns: 6/3; 36/3; 65/1
C:Superfamily: mammalian cytochrome-c oxidase chain VIIA
C:Keywords: liver; mitochondrion; oxidoreductase
F.1-23/Dominant: transit peptide (mitochondrion) #status predicted <TNP>
F.24-83/Product: cytochrome-c oxidase chain VIIA #status predicted <YAN>

Query Match 88.9%; Score 16; DB 2; Length 83;
Best Local Similarity 60.0%; Pred. No. 6e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
|||
DB 55 YRATL 59

RESULT 6
T14380
probable pollen coat protein 1 - turnip
C:Species: Brassica rapa (turnip)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T14380
R:Toriyama, K.; Hanaoka, K.; Okada, T.; Watanabe, M.
PNAS Lett. 424, 234-238, 1998
A:Title: Molecular cloning of a cDNA encoding a pollen extracellular protein as a pot
A:Reference number: Z18017; MUID:98198560
A:Accession: T14380
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-83 <TOR>
A:Cross-references: EMBL:AB010435; NID:g3062794; PIDN:BAA25682.1; PID:g3062795
A:Experimental source: anther
C:Genetics:
A:Gene: PEC-3

Query Match 88.9%; Score 16; DB 2; Length 83;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2002, 10:37:20 ; Search time 85.5 Seconds
(without alignments)
2.144 Million cell updates/sec

Title: US-09-281-760C-2

Perfect score: 18

Sequence: 1 YRXXL 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	16	88.9	68	1 VGC_BPAL3	P31279 bacteriophage
2	16	88.9	68	1 VGC_BPPIK	Q38037 bacteriophage
3	16	88.9	83	1 COXI_BOVIN	P13184 bos taurus
4	16	88.9	92	1 MOTT_HORSE	Q46617 equus caball
5	16	88.9	111	1 VP34_BPAPS	Q9t154 bacteriophage
6	16	88.9	115	1 MOTT_MACMU	Q18811 macaca mula
7	16	88.9	116	1 MOTT_FELCA	Q9xs62 felis silve
8	16	88.9	119	1 MOTT_PIG	P01307 sus scrofa
9	16	88.9	124	1 NU5C_PEA	Q32905 pisum sativ
10	16	88.9	129	1 RS9_BACSU	P21470 bacillus su
11	16	88.9	130	1 UCRC_SCHMA	Q01374 schistosoma
12	16	88.9	132	1 GCSH_SYNY3	P73560 synchocyst
13	16	88.9	133	1 MOTT_RABIT	P27114 oryctolagus
14	16	88.9	183	1 RL6_MYCGA	O52321 cyctobacter
15	16	88.9	185	1 AAC6_CITDI	P10051 citrobacter
16	16	88.9	188	1 VATE_TRETH	P74901 thermus aqu
17	16	88.9	194	1 RM06_PROMI	P46748 protheca
18	16	88.9	198	1 OPNR_AGRRA	P27872 deirococcus
19	16	88.9	206	1 MSRA_DETRA	Q9rtb6 deirococcus
20	16	88.9	208	1 RL13_CHISW	O48513 chlamydomon
21	16	88.9	210	1 SGCE_ECOLI	P39362 escherichia
22	16	88.9	213	1 RM06_SCHPO	O09865 schizosacch
23	16	88.9	214	1 VTI1_SCHPO	P78768 schizosacch
24	16	88.9	229	1 Y454_TREPA	O83467 treponema p
25	16	88.9	230	1 CUTI_FUSSC	O99174 fusarium so
26	16	88.9	230	1 CUTI_FUSSO	P00560 fusarium so
27	16	88.9	234	1 CITE_KLEPN	P52668 klebsiella
28	16	88.9	236	1 HO_PORPU	P51271 porphyra pu
29	16	88.9	239	1 RS3_SYNY3	P73314 synchocyst
30	16	88.9	245	1 ENDS_MYCLE	O9c692 mycobacteri
31	16	88.9	248	1 Y4EK_RHISN	P55434 rhizobium s
32	16	88.9	263	1 YEET_HUMAN	O95050 homo sapien
33	16	88.9	264	1 NNMT_MOUSE	O55239 mus musculu

34	16	88.9	264	1 YEET_MOUSE	P40936 mus musculu
35	16	88.9	269	1 MIND_GUTTH	O78436 guillierdia
36	16	88.9	271	1 ELHI_APLCA	P01362 aplysia cal
37	16	88.9	276	1 SSOC_BACSU	P40401 bacillus su
38	16	88.9	279	1 YEB8_YEAST	P39995 saccharomyc
39	16	88.9	293	1 VG11_BPBO3	Q37892 bacteriophage
40	16	88.9	296	1 KHEE_LACIA	O9c9d7 lactococcus
41	16	88.9	296	1 KHEE_LACIA	P52991 lactococcus
42	16	88.9	298	1 YSRK_CAEEL	Q19408 caenorhabdi
43	16	88.9	300	1 PPRD_DEIRA	O32504 deinooccus
44	16	88.9	310	1 S6PD_MALDO	P28475 malus domes
45	16	88.9	313	1 MPCI_ALCEU	P17295 alcaligenes
46	16	88.9	315	1 SR2A_PHYPO	P09352 physarum po
47	16	88.9	316	1 THER_BACTH	P00800 bacillus th
48	16	88.9	322	1 PTY_MORIA	P19257 moraxella l
49	16	88.9	324	1 SECF_RHOSH	O33568 rhodospirillum rubrum
50	16	88.9	325	1 HLBG_STAVU	Q07226 staphylococ

ALIGNMENTS

RESULT 1					
ID VGC_BPAL3	STANDARD;	PRT;	68 AA.		
AC P31279;					
DT 01-JUL-1993 (Rel. 26, Created)					
DT 01-JUL-1993 (Rel. 26, Last sequence update)					
DT 01-JUN-1994 (Rel. 29, Last annotation update)					
DE C PROTEIN.					
GN C.					
OS Bacteriophage alpha-3.					
OC Viruses; ssDNA viruses; Microviridae; Microvirus.					
OX NCBI_TaxID=10849;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE-92223109; PubMed-1532908;					
RA Kodaira K.-I., Nakano K., Okada S., Takeo A.;					
RT "Nucleotide sequence of the genome of the bacteriophage alpha 3:					
RT Interrelationship of the genome structure and the gene products with					
RL Biochim. Biophys. Acta 1130:277-288(1992).					
CC -1- FUNCTION: C PROTEIN IS ONE OF THE PROTEINS INVOLVED IN THE					
CC PRODUCTION AND PACKAGING OF VIRAL SINGLE-STRANDED DNA.					
CC -----					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC the European Bioinformatics Institute. There are no restrictions on its					
CC use by non-profit institutions as long as its content is in no way					
CC modified and this statement is not removed. Usage by and for commercial					
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC or send an email to license@sib-sib.ch).					
CC -----					
DR EMBL; X60322; CAA42877.1; -					
DR PIR; S22327; S22327.					
SQ SEQUENCE 68 AA; 8295 MW; 7F80D3EA2FBB4D4F CRC64;					

Query Match 88.9%; Score 16; DB 1; Length 68;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0;

QY 1 YRXXL 5					
DB 11 YRATL 15					
RESULT 2					
ID VGC_BPPIK	STANDARD;	PRT;	68 AA.		
AC Q38037;					
DT 01-NOV-1997 (Rel. 35, Created)					
DT 01-NOV-1997 (Rel. 35, Last sequence update)					

DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE C PROTEIN.
 GN C.
 OS Bacteriophage phi-K.
 CC Viruses; ssDNA viruses; Microviridae; Microvirus.
 OX NCBI_TaxID=10848;
 RN [1]
 RP SOURCE FROM N.A.
 RA Kodaira K.-I., Tadokoro H., Suzuki K., Oki M., Manto S., Taketo A.:
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: C PROTEIN IS ONE OF THE PROTEINS INVOLVED IN THE
 CC PRODUCTION AND PACKAGING OF VIRAL SINGLE-STRANDED DNA.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X60323; CAA42886.1; -
 DR SEQUENCE 68 AA; 8323 MW; 7F80D3EA38B4D4F CRC64;
 SQ
 QY 1 YRXXL 5
 DB 11 YRATL 15
 Query Match 88.9%; Score 16; DB 1; Length 68;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
 COX1_BOVIN STANDARD; PRT; 83 AA.
 ID COX1_BOVIN
 AC P13184;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIITA-LIVER/HEART, MITOCHONDRIAL
 DE PRECURSOR (EC 1.9.3.1) (CYTOCHROME C OXIDASE SUBUNIT VIITA-L) (VIITIC).
 GN COX7A2 OR COX7AL.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89366688; PubMed=2549516;
 RA Seelan R.S., Scheuner D., Lomax M.I., Grossman L.I.:
 RL "Nucleotide sequence of a cDNA for bovine cytochrome c oxidase
 RL subunit VIITA".
 RN Nucleic Acids Res. 17:6410-6410(1989).
 RN [2]
 RP REVISIONS: SEQUENCE FROM N.A.
 RA MEDLINE=92011761; PubMed=1717471;
 RA Seelan R.S., Grossman L.I.:
 RL "Cytochrome c oxidase subunit VIITA isoforms. Characterization and
 RL expression of bovine cDNAs".
 RN J. Biol. Chem. 266:19752-19757(1991).
 RN [3]
 RP SEQUENCE OF 24-60.
 RC TISSUE=Liver.
 RX MEDLINE=89000697; PubMed=2844245;
 RA Yamamura W., Zhang Y.-Z., Takamiya S., Capaldi R.A.:
 RT "Tissue-specific differences between heart and liver cytochrome c
 RT oxidase".
 RL Biochemistry 27:4909-4914(1988).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN

CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERROCYTOCHROME C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIITA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L09603; AAA18218.1; -
 DR EMBL: X15235; CAA3313.1; ALT_SEQ.
 DR PIR: B41034; B41034.
 DR PIR: C29968; C29968.
 DR InterPro: IPR003177; COX7A.
 DR Pfam: PF02238; COX7A; 1.
 KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
 FT TRANSIT 1 23
 FT CHAIN 24 83
 FT MITOCHONDRION.
 FT CYTOCHROME C OXIDASE POLYPEPTIDE
 FT VIITA-LIVER/HEART.
 FT AL -> NI (IN REF. 3).
 FT A -> V (IN REF. 3).
 FT L -> M (IN REF. 3).
 FT CONFLICT 52 53
 FT CONFLICT 57 57
 FT CONFLICT 59 59
 SQ SEQUENCE 83 AA; 9305 MW; 254D7610F2EF106F CRC64;
 QY 1 YRXXL 5
 DB 55 YRATL 59
 Query Match 88.9%; Score 16; DB 1; Length 83;
 Best Local Similarity 60.0%; Pred. No. 2.1e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
 MOT1_HORSE STANDARD; PRT; 92 AA.
 ID MOT1_HORSE
 AC O46617;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MOTILIN PRECURSOR [CONTAINS: MOTILIN, MOTILIN ASSOCIATED PEPTIDE
 DE (MAP)] (FRAGMENT).
 GN MNR.
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Duodenal mucosa.
 RC Huang Z., De Clercq P., Depoortere I., Peeters T.L.:
 RL "cDNA encoding motilin precursor from horse duodenum mucosa".
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE REGULATION OF
 CC INTERDIGESTIVE GASTROINTESTINAL MOTILITY AND INDIRECTLY CAUSES
 CC RHYTHMIC CONTRACTION OF DUODENAL AND COLONIC SMOOTH MUSCLE (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE MOTILIN FAMILY.
 CC -----
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:35:42 ; Search time 191.29 Seconds
(without alignments)
3.823 Million cell updates/sec

Title: US-09-281-760C-2
Perfect score: 18
Sequence: 1 YRXXL 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	88.9	44	8 P92073	P92073 euhadra her
2	16	88.9	56	3 Q9UT14	Q9UT14 schizosacch
3	16	88.9	63	2 P94133	P94133 actinobact
4	16	88.9	63	6 Q9TV14	Q9TV14 oryctolagus
5	16	88.9	66	5 Q9NM53	Q9NM53 leishmania
6	16	88.9	73	2 Q9F6T0	Q9F6T0 helicobacte
7	16	88.9	73	2 Q9EUA9	Q9EUA9 helicobacte
8	16	88.9	73	2 Q9EUA9	Q9EUA9 helicobacte
9	16	88.9	75	2 Q9X318	Q9X318 bacillus an
10	16	88.9	81	10 Q40745	Q40745 oryza sativ
11	16	88.9	83	10 Q64433	Q64433 brassica ra
12	16	88.9	83	10 Q9MB53	Q9MB53 brassica ra
13	16	88.9	83	10 Q9MB52	Q9MB52 brassica ju
14	16	88.9	83	10 Q9LDB24	Q9LDB24 brassica ca
15	16	88.9	90	12 Q41642	Q41642 human immun
16	16	88.9	93	3 Q9UV10	Q9UV10 glibberella
17	16	88.9	93	8 Q9MT19	Q9MT19 oenothera h
18	16	88.9	101	3 Q07236	Q07236 saccharomyc
19	16	88.9	102	1 Q9HQM0	Q9HQM0 halobacteri

20	16	88.9	102	10	Q9C8A2	Q9C8A2 arabidopsis
21	16	88.9	102	11	Q9QVZ1	Q9QVZ1 rattus sp.
22	16	88.9	108	5	Q61383	Q61383 papilio gla
23	16	88.9	112	2	Q9RS90	Q9RS90 deinococcus
24	16	88.9	113	13	Q918A6	Q918A6 meleagris g
25	16	88.9	114	2	P96462	P96462 salmonella
26	16	88.9	115	2	Q9MCS8	Q9MCS8 bacterioph
27	16	88.9	117	2	Q9Z5T2	Q9Z5T2 zymomonas m
28	16	88.9	118	10	Q65700	Q65700 arabidopsis
29	16	88.9	118	11	Q9DBE1	Q9DBE1 mus musculu
30	16	88.9	122	5	Q9GYZ6	Q9GYZ6 sanderia ma
31	16	88.9	126	2	Q9Z5Y0	Q9Z5Y0 frankia sp.
32	16	88.9	128	5	Q9NH50	Q9NH50 penaeus mon
33	16	88.9	128	10	Q9FGB4	Q9FGB4 arabidopsis
34	16	88.9	130	2	Q9RFJ7	Q9RFJ7 streptomyce
35	16	88.9	130	10	Q9M1M5	Q9M1M5 arabidopsis
36	16	88.9	131	1	Q27514	Q27514 methanobact
37	16	88.9	131	10	Q9SHW1	Q9SHW1 arabidopsis
38	16	88.9	139	2	Q68053	Q68053 rhodobacter
39	16	88.9	140	12	Q11312	Q11312 molluscum c
40	16	88.9	143	11	Q9D9X3	Q9D9X3 mus musculu
41	16	88.9	152	2	Q9S575	Q9S575 pseudomonas
42	16	88.9	156	1	Q9HRE9	Q9HRE9 halobacteri
43	16	88.9	159	2	Q91193	Q91193 pseudomonas
44	16	88.9	160	10	Q49380	Q49380 arabidopsis
45	16	88.9	165	10	Q9FGB2	Q9FGB2 arabidopsis
46	16	88.9	166	12	Q66019	Q66019 crinean-con
47	16	88.9	167	10	Q9LRT9	Q9LRT9 arabidopsis
48	16	88.9	169	5	Q61605	Q61605 drosophila
49	16	88.9	171	11	Q9CUN9	Q9CUN9 mus musculu
50	16	88.9	172	2	P97025	P97025 brevibacter

ALIGNMENTS

RESULT 1
ID P92073 PRELIMINARY; PRT; 44 AA.
AC P92073;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ATPASE SUBUNIT 6 (FRAGMENT).
OS Euhadra heriklotzi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
OC Helicacea; Bradybaenidae; Euhadra.
OX NCBI_TaxID=58912;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOPANCREAS;
RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
RA Watanabe K., Thomas R.H.;
DR EMBL: Z71697; CAA6374.1;
DR Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR Interpro: IPR000568; ATP_syn_A.
DR Pfam: PF00119; ATP_syn_A; 1.
FT Mitochondrion.
FT NON_TER
SQ SEQUENCE 44 AA; 5279 MW; 6EFB539307F2DF89 CRC64;

Query Match 88.9%; Score 16; DB 8; Length 44;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRXXL 5
DB 39 YRSSL 43

RESULT 2
ID Q9UT14 PRELIMINARY; PRT; 56 AA.
AC Q9UT14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE VERY HYPOTHEICAL PROTEIN.
GN SPAC9B9.17C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
NCBI_Taxid=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RT [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Barrett B.G., Rajandream M.A., Wood V.;
RA Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 299262; CAB58229.1; -;
SQ SEQUENCE 56 AA: 6413 MW: 48B23E9B5F2F2676 CRC64;

Query Match 88.9%; Score 16; DB 3; Length 56;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
DB 37 YRYYL 41

RESULT 3
ID P94133 PRELIMINARY; PRT; 63 AA.
AC P94133;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHEICAL 7.1 KDA PROTEIN (FRAGMENT).
OS Acinetobacter sp. ADP1.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
NCBI_Taxid=62977;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADP1;
RX MEDLINE=97440147; PubMed=9294455;
RA Williams P.A., Shaw L.E.;
RA "muck" a gene in Acinetobacter calcoaceticus ADP1 (BD413), encodes the
RT ability to grow on exogenous cis,cis-muconate as the sole carbon
RT source."
RL J. Bacteriol. 179:5935-5942(1997).
DR EMBL; U87258; AAC27119.1; -;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 63 AA: 7128 MW: 49B1579381B69B2 CRC64;

Query Match 88.9%; Score 16; DB 2; Length 63;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
DB 22 YRYYL 26

RESULT 4
ID Q9TV14 PRELIMINARY; PRT; 63 AA.
AC Q9TV14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PORCASSIUM CHANNEL KV4.2 (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutelia; Lagomorpha; Leporidae; Oryctolagus.
NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC Shi H., Wang Z.;
RT "Rabbit potassium channel KV4.2 mRNA, partial cds."
RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF085171; AAD49438.1; -;
DR InterPro; IPR003131; K_tetra.
DR Pfam; PF02214; K_tetra; 1.
KW Tonic channel.
FT NON_TER 63
SQ SEQUENCE 63 AA: 7091 MW: B23535CEB689CD7 CRC64;

Query Match 88.9%; Score 16; DB 6; Length 63;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
DB 22 YRYYL 26

RESULT 5
ID Q9NM53 PRELIMINARY; PRT; 66 AA.
AC Q9NM53;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HYPOTHEICAL 7.9 KDA PROTEIN (FRAGMENT).
GN IAW6.239.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_Taxid=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Murphy E., Quail M., Harris D., Rajandream M., Ivens A., Barrett B.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL160493; CAB97857.1; -;
KW Hypothetical protein.
FT NON_TER 66
SQ SEQUENCE 66 AA: 7876 MW: A3CA0216D54D3C73 CRC64;

Query Match 88.9%; Score 16; DB 5; Length 66;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
DB 60 YRSSL 64

RESULT 6
ID Q9F6T0 PRELIMINARY; PRT; 73 AA.
AC Q9F6T0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

XX Purificn. of human inducible nitric oxide synthase from cultured
 CC cells - using specific antibody directed against a C-terminal
 PT epitope

PS Example 3; Fig 2; 52pp; English.

XX This is the epitope of the human inducible nitric oxide synthase (hNOS)
 CC without the C-terminal leucine. The primary wild type antigen is given
 CC in AAW12317. It is shown that the C-terminal leucine of the epitope is
 CC required for antibody recognition by the ability of radiolabelled
 CC peptide to be displaced by unlabeled peptide, and by the specificity of
 CC the antibody to a C-terminal leucine. Antibodies raised against the
 CC primary antigen can be used to purify hNOS from cultured cells in a
 CC claimed method. Elevated levels of hNOS are implicated in a wide variety
 CC of diseases, particularly inflammatory conditions such as psoriasis,
 CC uveitis, rheumatoid arthritis and many others. The antibodies can be
 CC used to detect or quantify hNOS (by usual immunoassay or
 CC immunolocalisation techniques), also to evaluate the activity of hNOS
 CC modulators (which are potentially useful as therapeutic agents).

XX Sequence 9 AA:

Query Match 88.9%; Score 16; DB 18; Length 9;

Best Local Similarity 60.0%; Pred. No. 4.3e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
 II I
 Db 1 Yrasl 5

RESULT 2

ID AAW23311 standard; peptide: 10 AA.

XX AAW23311;

AC 30-MAR-1998 (first entry)

XX Human inducible nitric oxide synthase immunogenic peptide.

XX Inducible nitric oxide synthase; hNOS; endothelial nitric oxide synthase;
 KW eNOS; diagnosis; detection; inflammatory response.

XX Synthetic.

XX Homo sapiens.

XX MO9734014-A1.

XX 18-SEP-1997.

XX 14-MAR-1997; 97WO-US04293.

XX 15-MAR-1996; 96US-0013470.

XX (UYVA) UNIV YALE.

XX Sessa WC, Smith SD, Weiss RM, Wheeler MA;

XX WPI; 1997-470890/43.

XX Detection of inducible nitric oxide synthase - useful for monitoring
 PT levels over periods of time, or to diagnose disease associated with
 PT hNOS levels

PS Disclosure: Page 9; 32pp; English.

XX This sequence is an immunogenic peptide for detecting inducible nitric
 CC oxide synthase (hNOS) immunoreactivity which is used in a novel method
 CC to detect hNOS in a biological sample. The level of hNOS is related to
 CC an inflammatory response, e.g. infection mediated by bacteria, yeast or

CC a virus, organ transplant rejection, rheumatoid arthritis, interstitial
 CC cystitis or cancer. By monitoring levels of hNOS over a period of time
 CC it is possible to diagnose a disease or condition associated with
 CC increased or decreased hNOS.

XX Sequence 10 AA:

Query Match 88.9%; Score 16; DB 18; Length 10;

Best Local Similarity 60.0%; Pred. No. 2.2e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXXL 5
 II I
 Db 1 Yrasl 5

RESULT 3

ID AAW12319 standard; Peptide; 10 AA.

XX AAW12319;

XX 20-OCT-1997 (first entry)

XX Radiolabelled hNOS C-terminal immunogenic peptide.

XX C-terminal; epitope; human; inducible nitric oxide synthase; hNOS;
 KW antibody; purification; detection; inflammatory; psoriasis; uveitis;
 KW rheumatoid arthritis.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note="125-I labeled Tyrosine"

FT Peptide 4..10 /note="primary antigen"

FT Modified-site 10 /note="required for antibody recognition; optionally
 FT amidated in sensitivity assay"

XX W09639858-A1.

XX 19-DEC-1996.

XX 03-JUN-1996; 96WO-US08447.

XX 07-JUN-1995; 95US-0485075.

XX (MERI) MERCK & CO INC.

XX Calaycay JR, Mumford RA, Schmidt JA, Weidner JR;

XX WPI; 1997-108622/10.

XX Purificn. of human inducible nitric oxide synthase from cultured
 CC cells - using specific antibody directed against a C-terminal
 PT epitope
 PS Example 3; Page 19; 52pp; English.

XX This sequence is a synthetic radio-iodinated peptide based on a C-
 CC terminal epitope of human inducible nitric oxide synthase (hNOS). It
 CC was used to generate a standard curve in a competitive radioimmunoassay
 CC for hNOS products. It was shown that the C-terminal leucine is required
 CC for antibody recognition by the ability of the radiolabelled peptide to
 CC be displaced by unlabeled peptide. The specificity of the antibody to a
 CC C-terminal leucine was also shown with use of peptides having amino acid
 CC substitutions/modifications at the C-terminus (see AAW12320-22).
 CC Antibodies raised against the primary antigen can be used to purify hNOS
 CC from cultured cells in a claimed method. Elevated levels of hNOS are
 CC implicated in a wide variety of diseases, particularly inflammatory

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:15:54 ; Search time 94.43 Seconds
(without alignments)
1.192 Million cell updates/sec

Title: US-09-281-760C-2
Perfect score: 18
Sequence: 1 YRXXL 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	88.9	13	4	US-09-461-697-318
2	16	88.9	30	4	US-09-461-697-314
3	16	88.9	32	2	US-08-606-143-38/
4	16	88.9	35	2	US-08-807-332B-9
5	16	88.9	35	4	US-09-338-876-9
6	16	88.9	40	1	US-08-735-963-3
7	16	88.9	40	2	US-09-105-057-3
8	16	88.9	40	4	US-09-304-214-3
9	16	88.9	48	2	US-08-637-759B-480
10	16	88.9	48	3	US-08-871-355A-480
11	16	88.9	113	4	US-09-284-033-7
12	16	88.9	113	4	US-08-729-834B-7
13	16	88.9	119	4	US-09-046-479-4
14	16	88.9	190	2	US-08-606-143-37
15	16	88.9	192	1	US-08-735-963-2
16	16	88.9	192	2	US-09-105-057-2
17	16	88.9	192	4	US-09-304-214-2
18	16	88.9	200	2	US-08-606-143-42
19	16	88.9	208	2	US-08-606-143-40
20	16	88.9	208	2	US-08-606-143-41
21	16	88.9	208	2	US-08-606-143-43
22	16	88.9	240	1	US-08-261-822A-82
23	16	88.9	240	5	PCT-US95-07744A-82
24	16	88.9	243	4	US-09-188-930-295
25	16	88.9	243	4	US-09-140-804-2
26	16	88.9	245	2	US-08-685-992-26
27	16	88.9	245	2	US-09-144-925-26

28	16	88.9	310	4	US-09-166-412-4	Sequence 4, Appl
29	16	88.9	316	1	US-08-038-932B-1	Sequence 1, Appl
30	16	88.9	316	1	US-08-656-349-1	Sequence 1, Appl
31	16	88.9	316	3	US-08-682-643-4	Sequence 4, Appl
32	16	88.9	316	4	US-09-104-623A-5	Sequence 5, Appl
33	16	88.9	362	1	US-08-415-751-35	Sequence 35, Appl
34	16	88.9	392	2	US-08-282-197C-60	Sequence 60, Appl
35	16	88.9	396	4	US-09-046-992-4	Sequence 4, Appl
36	16	88.9	420	1	US-08-391-259-2	Sequence 2, Appl
37	16	88.9	420	1	US-08-391-259-7	Sequence 7, Appl
38	16	88.9	420	1	US-08-391-259-10	Sequence 10, Appl
39	16	88.9	420	1	US-08-391-259-11	Sequence 11, Appl
40	16	88.9	420	2	US-08-839-425-2	Sequence 2, Appl
41	16	88.9	420	2	US-08-839-425-7	Sequence 7, Appl
42	16	88.9	420	2	US-08-839-425-10	Sequence 10, Appl
43	16	88.9	420	2	US-08-839-425-11	Sequence 11, Appl
44	16	88.9	436	1	US-08-021-601-6	Sequence 6, Appl
45	16	88.9	436	1	US-08-082-849B-6	Sequence 6, Appl
46	16	88.9	456	5	PCT-US94-01624-6	Sequence 6, Appl
47	16	88.9	462	2	US-08-484-438-42	Sequence 42, Appl
48	16	88.9	472	1	US-08-021-601-8	Sequence 8, Appl
49	16	88.9	472	1	US-08-082-849B-8	Sequence 8, Appl
50	16	88.9	472	5	PCT-US94-01624-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-461-697-318
; Sequence 318, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Putnam, Kasuri
; APPLICANT: Kalz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 318
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-318

Query Match 88.9%; Score 16; DB 4; Length 13;
Best Local Similarity 60.0%; Pred. No. 73;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRXXL 5
Db 2 YRSSL 6
US-09-461-697-314
; Sequence 314, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth

APPLICANT: Portbury, Stuart D.
APPLICANT: Putnam, Kasturi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
FILE REFERENCE: 10001-005-999
CURRENT FILING DATE: 1999-12-14
CURRENT APPLICATION NUMBER: US/09/461,697
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 314
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-09-461-697-314

Query Match 88.9%; Score 16; DB 4; Length 30;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRXL 5
Db 19 YRSL 23

RESULT 3
US-08-606-143-38
Sequence 38, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-38

Query Match 88.9%; Score 16; DB 2; Length 32;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 YRXL 5
Db 16 YRSL 20

RESULT 4
US-08-807-332B-9
Sequence 9, Application US/0807332B
Patent No. 5959074
GENERAL INFORMATION:
APPLICANT: Dreyfus, David H.
APPLICANT: Gelfand, Erwin W.
TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,332B
FILING DATE: 28-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-39
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-807-332B-9

Query Match 88.9%; Score 16; DB 2; Length 35;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRXL 5
Db 30 YRSL 34

RESULT 5
US-09-338-876-9
Sequence 9, Application US/09338876
Patent No. 6187584
GENERAL INFORMATION:
APPLICANT: Dreyfus, David H.
APPLICANT: Gelfand, Erwin W.
TITLE OF INVENTION: PRODUCTS AND PROCESSES FOR REGULATION OF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:17:56 ; Search time 102.84 Seconds
(without alignments)
5.926 Million cell updates/sec

Title: US-09-281-760C-3

Perfect score: 24

Sequence: 1 LXXYRXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	83.3	384	2	S34816
2	20	83.3	412	2	T21419
3	19	79.2	152	2	T44544
4	19	79.2	208	2	T34544
5	19	79.2	226	2	G81894
6	19	79.2	226	2	D81125
7	19	79.2	258	2	H83373
8	19	79.2	324	2	T09873
9	19	79.2	328	2	B75403
10	19	79.2	354	2	B65219
11	19	79.2	354	2	G86104
12	19	79.2	366	2	D83224
13	19	79.2	377	2	T05354
14	19	79.2	377	2	C83372
15	19	79.2	401	2	S16893
16	19	79.2	440	2	T47906
17	19	79.2	487	2	T32941
18	19	79.2	508	2	T50180
19	19	79.2	545	1	R8B6BM
20	19	79.2	566	2	S35231
21	19	79.2	581	2	B72221
22	19	79.2	597	2	T10034
23	19	79.2	601	2	T49752
24	19	79.2	710	2	S26006
25	19	79.2	790	2	D83011
26	19	79.2	909	2	A75337
27	19	79.2	1067	2	T39449
28	19	79.2	1388	2	A53117
29	18	75.0	48	2	B86373

30	18	75.0	69	2	S44888	ZK112.6 protein -
31	18	75.0	77	2	C70967	hypothetical prote
32	18	75.0	96	2	T17209	hypothetical prote
33	18	75.0	98	2	S35469	NADH dehydrogenase
34	18	75.0	102	2	C96595	hypothetical prote
35	18	75.0	103	2	T24311	hypothetical prote
36	18	75.0	106	2	T48070	hypothetical prote
37	18	75.0	109	2	C85718	probable tail comp
38	18	75.0	109	2	C85742	probable tail comp
39	18	75.0	109	2	C85817	hypothetical prote
40	18	75.0	113	2	T15406	hypothetical prote
41	18	75.0	113	1	MSPG	motilin precursor
42	18	75.0	133	1	S24315	hypothetical prote
43	18	75.0	144	2	G70023	hypothetical prote
44	18	75.0	166	2	G83176	hypothetical prote
45	18	75.0	175	2	T13067	hypothetical prote
46	18	75.0	176	2	F71321	conserved hypotet
47	18	75.0	190	2	B42957	iron-sulfur protei
48	18	75.0	192	2	F70359	hypothetical prote
49	18	75.0	197	2	T47159	hypothetical prote
50	18	75.0	198	1	A57987	nifg protein - Esc

ALIGNMENTS

RESULT 1
S34816
nitrogenase cofactor synthesis protein nifs - Rhodobacter capsulatus
N:contains: L-cysteine sulfotransferase (EC 2.8.1.1-)
C:Species: Rhodobacter capsulatus
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-Dec-1999
C:Accession: S34816
R:Massepohl, B.; Angermueller, S.; Hennecke, S.; Huebner, P.; Moreno-Vivian, C.; Klipp
Mol. Gen. Genet. 238, 369-382, 1993
A:Title: Nucleotide sequence and genetic analysis of the Rhodobacter capsulatus ORF6-
A:Reference number: S34814; MUID:93261420
A:Accession: S34816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-384 <MAS>
A:Cross-references: EMBL:X68444; NID:g297915; PIDN:CAA48487.1; PID:g297918
C:Genetics:
A:Gene: nifs
C:Superfamily: nitrogen fixation protein nifs
C:Keywords: phosphoprotein; pyridoxal phosphate; sulfotransferase
F:203/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted
F:325/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 83.3% Score 20; DB 2; Length 384;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LXXYRXXL 8
Db 133 LAAVRAAL 140

RESULT 2
T21419
hypothetical protein F26E4.13 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21419
R:Lighting, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: T21419
A:Accession: T21419
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-412 <MIL>
A:Cross-references: EMBL:Z81070; PIDN:CAB03005.1; GSPDB:GND00019; CESP:F26E4.13

A:Experimental source: clone F26E4

C:Genetics:

A:Gene: CDS:F26E4.13

A:Map position: 1

A:Insertions: 359/2; 400/3

Query Match 83.3%; Score 20; DB 2; Length 412;

Best Local Similarity 50.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXL 8

DB 50 LARYRAL 57

RESULT 3

Conserved hypothetical protein PA0621 [Imported] - *Pseudomonas aeruginosa*

C:Species: *Pseudomonas aeruginosa*

C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Dec-2000

C:Accession: T44544; C83567

R:Nakayama, K.; Takashima, K.; Ishihara, H.; Shinomiya, T.; Kageyama, M.; Kanaya, S.; Oh

submitted to the EMBL Data Library, August 1999

A:Description: Genetic relationship between bacteriophages and bacteriophages.

A:Reference number: 222790

A:Accession: T44544

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-152 <NNK>

A:Cross-references: EMBL:AB030825; PIDN:BAA83159.1

A:Experimental source: strain PA01

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Loiy, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337

A:Accession: C83567

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-152 <STO>

A:Cross-references: GB:AE004498; GB:AE004091; NID:g9946491; PIDN:AG04010.1; GSPDB:GN004

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA0621

Query Match 79.2%; Score 19; DB 2; Length 152;

Best Local Similarity 50.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXL 8

DB 117 LMSYRSL 124

RESULT 4

hypothetical protein SCE94.30c - *Streptomyces coelicolor*

C:Species: *Streptomyces coelicolor*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36390

R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A:Reference number: Z21573

A:Accession: T36390

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-208 <OLI>

A:Cross-references: EMBL:AL049628; PIDN:CA040879.1; GSPDB:GN00070; SCOEDB:SCE94.30c

A:Experimental source: strain A5(2)

C:Genetics:

A:Gene: SCOEDB:SCE94.30c

Query Match 79.2%; Score 19; DB 2; Length 208;

Best Local Similarity 50.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXL 8

DB 67 LARYRAL 74

RESULT 5

probable integral membrane protein NMA1265 [Imported] - *Neisseria meningitidis* (strain

C:Species: *Neisseria meningitidis*

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: G81894

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churche, C.; Klee, S.R.; Mo

rolyd, S.; Jagers, K.; Leather, S.; Mout, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491

A:Reference number: A81775; MUID:2022556

A:Accession: G81894

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <PAR>

A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA084520.1; PID:g737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1265

Query Match 79.2%; Score 19; DB 2; Length 226;

Best Local Similarity 50.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXL 8

DB 35 LARYRAL 42

RESULT 6

hypothetical protein NMB1066 [Imported] - *Neisseria meningitidis* (strain MC58 serogro

C:Species: *Neisseria meningitidis*

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: D81125

R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.

rt, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappaport, R.

A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755

A:Accession: D81125

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <TEP>

A:Cross-references: GB:AE002457; GB:AE002098; NID:g7226304; PIDN:AA04162.1; PID:g722

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1066

Query Match 79.2%; Score 19; DB 2; Length 226;

Best Local Similarity 50.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXL 8

DB 35 LARYRAL 42

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:37:23 ; Search time 85.5 Seconds
(without alignments)
3.431 Million cell updates/sec

Title: US-09-281-760c-3
Perfect score: 24
Sequence: 1 LXXYRXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	83.3	384 1 NIFS_RHOCA	007177 rhodobacter
2	20	83.3	412 1 RNC_CAEEL	001326 caenorhabdi
3	19	79.2	38 1 CRRP_CANFG	P81033 cancer pagu
4	19	79.2	208 1 RL13_CHLSW	O48513 chlamydomon
5	19	79.2	263 1 YEWT_HUMAN	O95050 homo sapien
6	19	79.2	354 1 PHNI_ECOLI	P16687 escherichia
7	19	79.2	368 1 PHNI_RHIME	O52986 rhizobium m
8	19	79.2	441 1 PUS6_ARATH	P45432 arabidopsis
9	19	79.2	544 1 RPO_BPM52	P00585 bacteriopho
10	19	79.2	566 1 HOXX_BRAJA	P31907 bradyrhizob
11	19	79.2	1004 1 EPA8_MOUSE	O09127 mus musculu
12	19	79.2	1067 1 IMB4_SCHPO	P39059 homo sapien
13	19	79.2	1388 1 CAIE_HUMAN	P34615 caenorhabdi
14	18	75.0	69 1 YOC6_CAEEL	O46517 equus cabal
15	18	75.0	92 1 MOTI_HORSE	P34193 crossostoma
16	18	75.0	98 1 NDLM_CROLA	O11192 caenorhabdi
17	18	75.0	113 1 YX21_CAEEL	O18811 macaca mula
18	18	75.0	115 1 MOTI_MACMU	O98522 felis silve
19	18	75.0	116 1 MOTI_FELCA	P01307 sus scrofa
20	18	75.0	119 1 MOTI_PIG	O01374 schistosoma
21	18	75.0	130 1 UCR6_SCHMA	P27114 oryctolagus
22	18	75.0	133 1 MOTI_RABIT	P31894 rhodospiril
23	18	75.0	190 1 COOF_RHORU	O66506 aquifex aeo
24	18	75.0	192 1 Y678_AQUAE	P97463 mus musculu
25	18	75.0	195 1 NRTN_MOUSE	O99718 homo sapien
26	18	75.0	197 1 NREG_HUMAN	P32712 escherichia
27	18	75.0	198 1 ERT3_MOUSE	P48299 mus musculu
28	18	75.0	214 1 NNTT_MOUSE	O55239 mus musculu
29	18	75.0	264 1 XERD_SALTY	P55889 salmonella
30	18	75.0	298 1 YSMK_CAEEL	O19408 caenorhabdi
31	18	75.0	325 1 DBP_HUMAN	O10566 homo sapien
32	18	75.0	325 1 DBP_MOUSE	O60925 mus musculu
33	18	75.0	325 1 DBP_MOUSE	O60925 mus musculu

ALIGNMENTS

RESULT	ID	STANDARD	PRT	384 AA.
1	NIFS_RHOCA			
AC	007177			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CYSTEINE DESULFURASE (EC 4.4.1.-) (NITROGENASE METALLOCLUSTERS BIOSYNTHESIS PROTEIN NIFS).			
GN	NIFS.			
OS	Rhodobacter capsulatus (Rhodospseudomonas capsulata).			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;			
OC	Rhodobacter.			
OX	NCBI_TaxID=1061;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=B10;			
RA	MEDLINE=93261420; PubMed=8492805;			
RA	Moreno-Vivian C, Klipp W.;			
RT	"Nucleotide sequence and genetic analysis of the Rhodobacter capsulatus ORF-nl01 SVW gene region: possible role of Nlfw in homocitrate processing.";			
RT	Mol. Gen. Genet. 238:369-382(1993).			
RL	-1- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY SIMILARITY).			
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X68444; CAA8487.1; -			
DR	PIR; S34816; S34816.			
DR	InterPro; IPR000192; Aminotransf_class-V.			
DR	PIfam; PF00266; aminotran_5; 1.			
DR	PROSITE; PS00595; AA_TRANSFER_CLASS_5; 1.			
KW	Nitrogen fixation; Lyase; Pyridoxal phosphate.			
FT	BINDING 203 205 PYRIDOXAL-PHOSPHATE (BY SIMILARITY).			
FT	ACT SITE 325 325 BY SIMILARITY.			
SQ	SEQUENCE 384 AA: 40282 MW; C2CA282D80A8391 CRC64;			

34	18	75.0	325 1 DBP_RAT	P16443 rattus norv
35	18	75.0	340 1 ENDR_PAEPO	P27871 paenibacill
36	18	75.0	355 1 FKB8_HUMAN	Q14318 homo sapien
37	18	75.0	355 1 FKB8_MOUSE	O35465 mus musculu
38	18	75.0	364 1 DRG2_HUMAN	P55039 mus musculu
39	18	75.0	364 1 DRG2_MOUSE	O9qxb9 mus musculu
40	18	75.0	393 1 YWCF_BACSU	P38604 bacillus su
41	18	75.0	419 1 CTE1_MOUSE	O35137 mus musculu
42	18	75.0	419 1 CTE1_RAT	O88267 rattus norv
43	18	75.0	421 1 PTE2_HUMAN	P49753 homo sapien
44	18	75.0	432 1 PTE2_MOUSE	O9qyr7 mus musculu
45	18	75.0	439 1 V412_ARATH	O04658 arabidopsis
46	18	75.0	431 1 SUN_HAEIN	P44788 haemophilus
47	18	75.0	453 1 MTE1_MOUSE	O9qyr9 mus musculu
48	18	75.0	453 1 MTE1_RAT	O55171 rattus norv
49	18	75.0	461 1 MYH_SCHPO	Q10159 schizosacch
50	18	75.0	478 1 HLYD_PASHA	P16534 pasteurella

Query Match 83.3%; Score 20; DB 1; Length 384;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXXL 8
DB 133 LAAYRAL 140

RESULT 2

RNC_CAEEL STANDARD; PRT; 412 AA.

AC 001326;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE RIBONUCLEASE III (EC 3.1.26.3) (RNASE IIII).
EN F26E4.13;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Lightning J.;

RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOSPHO-MONESTER.
CC -1- SIMILARITY: BELONGS TO THE RNASE III FAMILY.
CC -1- SIMILARITY: CONTAINS 1 DBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.

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DR EMBL: Z81070; CAB03005.1;
DR WormPep: F26E4.13; CE09697.
DR InterPro: IPR001159; DS_RPD.
DR InterPro: IPR000999; RNase_3.
DR Pfam: PR00035; dsrm; 1.
DR SMART: SM00358; DSRM; 1.
DR SMART: SM00355; RIBOC_2.
DR PROSITE: PS00137; DS_RPD; 1.
DR PROSITE: PS00137; RNase_3_1; 2.
DR PROSITE: PS0142; RNase_3_2; 2.
KW Hypothetical protein; Hydrolase; Nuclease; Endonuclease.
FT DOMAIN 313 388 DSRM.
SQ SEQUENCE 412 AA; 47087 MW; E0840881AB87AF84 CRC64;

Query Match 83.3%; Score 20; DB 1; Length 412;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXXL 8
DB 50 LAAYRAL 57

RESULT 3

CPRP_CANPG STANDARD; PRT; 38 AA.

AC P81033;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CHH PRECURSOR RELATED PEPTIDE (CPRP).
OS Cancer pagurus (Rock crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Cancroidea; Cancridae; Cancer.
OX NCBI_TaxID=6755;
RN 11
RP SEQUENCE.

RC TISSUE=Stomach gland;
RX MEDLINE=99025664; PubMed=9809792;
RA Chung J S, Wilkinson M C, Webster S G;
RT "Amino acid sequences of both isoforms of crustacean hyperglycemic hormone (CHH) and corresponding precursor-related peptide in Cancer pagurus";
RL Regul. Pept. 77:17-24(1998).
CC -1- TISSUE SPECIFICITY: PRODUCED BY THE MEDULLA TERMINALIS X-ORGAN IN THE ESTRAUS AND TRANSPORTED TO THE STOMACH GLAND WHERE IT IS STORED AND RELEASED.
CC KW Neuropeptide; Hormone.
SQ SEQUENCE 38 AA; 3969 MW; C979C87EE31AB90 CRC64;

Query Match 79.2%; Score 19; DB 1; Length 38;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYRXXL 8
DB 13 LASYRAL 20

RESULT 4

RL13_CHL3W STANDARD; PRT; 208 AA.

AC 048513;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 60S RIBOSOMAL PROTEIN L13 (BCL1 PROTEIN HOMOLOG).
EN RPL13 OR BCL1.
OS Chlamydomonas sp. (strain W80).
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=103365;
RN 11
RP SEQUENCE FROM N.A.

RA Kanaboshi H., Ikeda K., Miyasaka H.;
RT "Isolation of several anti-stress genes from the halotolerant green alga Chlamydomonas by a simple functional expression screening in E. coli";
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE L13E FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL: AB009086; BAA23724.1;
DR Medel: 27085; Chlsp: 2745; 27085.
DR InterPro: IPR001380; Ribosomal_L13E.
DR Pfam: PF01294; Ribosomal_L13e; 1.
DR Pfam: PD004443; Ribosomal_L13e; 1.
DR PROSITE: PS01104; RIBOSOMAL_L13E; 1.
KW Ribosomal protein.
SQ SEQUENCE 208 AA; 23545 MW; F9BB54E2550EA43B CRC64;

Query Match 79.2%; Score 19; DB 1; Length 208;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2002, 10:35:46 ; Search time 191.29 Seconds
(without alignments)
6.117 Million cell updates/sec

Title: US-09-281-760c-3
Perfect score: 24
Sequence: 1 LXXYXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP. Archaea: *
2: SP. Bacteria: *
3: SP. Fungi: *
4: SP. Human: *
5: SP. Invertebrate: *
6: SP. Mammal: *
7: SP. MHC: *
8: SP. Organelle: *
9: SP. Phage: *
10: SP. Plant: *
11: SP. Rodent: *
12: SP. Virus: *
13: SP. Vertebrate: *
14: SP. Unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	83.3	315	4 Q9H4J8	Q9H4J8 homo sapien
2	20	83.3	331	4 O15405	O15405 homo sapien
3	20	83.3	480	2 Q9F2U5	Q9F2U5 streptomyce
4	20	83.3	526	4 Q94900	Q94900 homo sapien
5	20	83.3	656	12 Q9DWC3	Q9DWC3 rat cytochrome
6	20	83.3	860	5 Q9U9Q8	Q9U9Q8 caenorhabditis
7	19	79.2	139	2 Q9RD00	Q9RD00 streptomyce
8	19	79.2	152	2 Q9S575	Q9S575 pseudomonas
9	19	79.2	197	2 Q53172	Q53172 rhodospirillum rubrum
10	19	79.2	208	2 Q9X8N5	Q9X8N5 streptomyce
11	19	79.2	226	2 Q9U2G5	Q9U2G5 neisseria meningitidis
12	19	79.2	226	2 Q9JUL0	Q9JUL0 neisseria meningitidis
13	19	79.2	258	2 Q911U7	Q911U7 pseudomonas
14	19	79.2	258	10 Q9XIC2	Q9XIC2 arabidopsis
15	19	79.2	263	4 Q9UH00	Q9UH00 homo sapien
16	19	79.2	263	4 Q9UR74	Q9UR74 homo sapien
17	19	79.2	263	6 Q97972	Q97972 oryctolagus
18	19	79.2	324	10 Q23954	Q23954 gossypium hirsutum
19	19	79.2	328	2 Q9RUL5	Q9RUL5 deinococcus

20	19	79.2	366	2 Q9HYM3	Q9HYM3 pseudomonas
21	19	79.2	377	2 Q911T4	Q911T4 pseudomonas
22	19	79.2	377	10 Q9SUU8	Q9SUU8 arabidopsis
23	19	79.2	401	2 Q48910	Q48910 mycobacterium
24	19	79.2	403	2 Q52629	Q52629 paracoccus
25	19	79.2	438	10 Q9FG39	Q9FG39 arabidopsis
26	19	79.2	440	10 Q9M2E9	Q9M2E9 arabidopsis
27	19	79.2	441	10 Q9C5F0	Q9C5F0 arabidopsis
28	19	79.2	487	5 Q45012	Q45012 caenorhabditis
29	19	79.2	508	3 Q9P7S7	Q9P7S7 schizosaccharomyces
30	19	79.2	523	5 Q16432	Q16432 geodia cydonia
31	19	79.2	525	12 Q89175	Q89175 rice grassy
32	19	79.2	525	12 Q9QNA1	Q9QNA1 rice grassy
33	19	79.2	525	12 Q9ELT1	Q9ELT1 rice grassy
34	19	79.2	526	9 Q9T1C5	Q9T1C5 enterobacter
35	19	79.2	566	5 Q9W243	Q9W243 drosophila
36	19	79.2	581	2 Q9X230	Q9X230 thermotoga
37	19	79.2	597	2 Q93086	Q93086 mycobacterium
38	19	79.2	597	2 Q9CDD7	Q9CDD7 mycobacterium
39	19	79.2	659	10 Q9FV60	Q9FV60 zea mays
40	19	79.2	693	8 Q9TK79	Q9TK79 calyptridium
41	19	79.2	706	2 Q9A2Q2	Q9A2Q2 caulobacter
42	19	79.2	710	8 Q35064	Q35064 marchantia
43	19	79.2	720	12 Q9DT76	Q9DT76 it virus
44	19	79.2	732	8 Q9TUS3	Q9TUS3 pentas lance
45	19	79.2	748	12 Q9D781	Q9D781 it virus
46	19	79.2	790	2 Q9HU93	Q9HU93 pseudomonas
47	19	79.2	853	4 Q9P269	Q9P269 homo sapien
48	19	79.2	859	2 Q33828	Q33828 thioabacillus
49	19	79.2	909	2 Q9RT44	Q9RT44 deinococcus
50	19	79.2	963	2 Q06458	Q06458 thermus aqu

ALIGNMENTS

RESULT 1
ID Q9H4J8 PRELIMINARY: PRT; 315 AA.
AC Q9H4J8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE D11108D11.2 (NOVEL HMG (HIGH MOBILITY GROUP) BOX PROTEIN SIMILAR TO KIAA0737, KIAA0808 AND TNRC9 (CAGP9)) (FRAGMENT).
GN D11108D11.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP CLARK G.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL034419; CAB81660.1; -
DR InterPro: IPR000135; Highmobility_12.
DR InterPro: IPR000910; HMG_12_box.
DR InterPro: IPR002965; P-rich_extensn.
DR Pfam: PF00505; HMG_box; 1.
DR PRINTS: PR00886; HIGHMOBILITY12.
DR PRINTS: PR01217; PRICHTEXTENS.
DR SMART: SM00398; HMG; 1.
FT NON_TER 1
FT NON_TER 315
SQ SEQUENCE 315 AA; F77A3178A48A27D5 CRC64;

Query Match 83.3%; Score 20; DB 4; Length 315;
Best Local Similarity 50.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0;
Gaps 0;

QY 1 LXXYXXL 8
| | |

Db 173 LAAYRASL 180

RESULT 2

ID 015405 PRELIMINARY: PRT: 331 AA.

AC 015405.

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE CAG9 (FRAGMENT).

GN CAG9.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=97369492; PubMed=9225980;

RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,

RT Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;

RL "CDNAs with long CAG trinucleotide repeats from human brain.";

DR EMBL: U80736; AAB91435.1; "

DR HSSP: P07155; IHMF.

DR InterPro: IPR000135; Highmobility_12.

DR InterPro: IPR000910; HMG_box; 1.

DR Pfam: PF00505; HMG_box; 1.

DR PRINTS: PR00886; HIGHMOBLTY12.

DR SMART: SM00398; HMG; 1.

FT NON_TER

SQ SEQUENCE 331 AA: 37161 MW: 7100E4BFA10766B CRC64;

Query Match 83.3%; Score 20; DB 4; Length 331;

Best Local Similarity 50.0%; Pred. No. 8.2e+02;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYXXL 8

Db 74 LAAYRASL 81

RESULT 3

ID 09F2U5 PRELIMINARY: PRT: 490 AA.

AC 09F2U5.

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE PUTATIVE ATP-BINDING PROTEIN.

GN SC039.17C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Brown S.P., Harris D.;

RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RC MEDLINE=97000351; PubMed=8843436;

RA Redelbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,

Kinsahl.H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RT Mol. Microbiol. 21:77-96(1996).

DR EMBL: AL392146; CAC08270.1; "

KW ATP-binding.

SQ SEQUENCE 490 AA: 53788 MW: 46BCD7DAC178FBAB CRC64;

Query Match 83.3%; Score 20; DB 2; Length 490;

Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYXXL 8

Db 374 LAAYRASL 381

RESULT 4

ID 094900 PRELIMINARY: PRT: 526 AA.

AC 094900.

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE KIA0808 PROTEIN.

GN KIA0808.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=9087487; PubMed=9872452;

RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A.,

RT Kotani H., Nomura N., Ohara O.;

RL "Prediction of the coding sequences of unidentified human genes. XI.

The complete sequences of 100 new cDNA clones from brain which code

for large proteins in vitro.";

DR EMBL: AB018351; BAA34528.1; "

DR HSSP: P07155; IHMF.

DR InterPro: IPR000135; Highmobility_12.

DR InterPro: IPR000910; HMG_box; 1.

DR Pfam: PF00505; HMG_box; 1.

DR PRINTS: PR00886; HIGHMOBLTY12.

DR SMART: SM00398; HMG; 1.

SQ SEQUENCE 526 AA: 57513 MW: 5AE4C5B07F2EB8FF CRC64;

Query Match 83.3%; Score 20; DB 4; Length 526;

Best Local Similarity 50.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LXXYXXL 8

Db 325 LAAYRASL 332

RESULT 5

ID 09DMC3 PRELIMINARY: PRT: 656 AA.

AC 09DMC3.

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE PR77.

GN R77.

OS Rat cytomegalovirus (strain Mastricht).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Betaherpesvirinae; Muromegalovirus.

OX NCBI_TaxID=79700;

RN [1]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:14:08 ; Search time 158.02 Seconds
(without alignments)
3.750 Million cell updates/sec

Title: US-09-281-760c-3
Perfect score: 24
Sequence: 1 LXXYRXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: A.GeneSeq.1101.*
2: /SIDS1/gcgdata/geneSeq/geneSeq/AA1980.DAT.*
3: /SIDS1/gcgdata/geneSeq/geneSeq/AA1981.DAT.*
4: /SIDS1/gcgdata/geneSeq/geneSeq/AA1982.DAT.*
5: /SIDS1/gcgdata/geneSeq/geneSeq/AA1983.DAT.*
6: /SIDS1/gcgdata/geneSeq/geneSeq/AA1984.DAT.*
7: /SIDS1/gcgdata/geneSeq/geneSeq/AA1985.DAT.*
8: /SIDS1/gcgdata/geneSeq/geneSeq/AA1986.DAT.*
9: /SIDS1/gcgdata/geneSeq/geneSeq/AA1987.DAT.*
10: /SIDS1/gcgdata/geneSeq/geneSeq/AA1988.DAT.*
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22: /SIDS1/gcgdata/geneSeq/geneSeq/AA2000.DAT.*
23: /SIDS1/gcgdata/geneSeq/geneSeq/AA2001.DAT.*
24: /SIDS1/gcgdata/geneSeq/geneSeq/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	83.3	388	22	AA1453
2	20	83.3	576	22	AA13667
3	19	79.2	42	22	AA14043
4	19	79.2	42	22	AA14043
5	19	79.2	42	22	AA14043
6	19	79.2	176	21	AA14043
7	19	79.2	180	22	AA14043
8	19	79.2	181	20	AA14043
9	19	79.2	181	20	AA14043
10	19	79.2	191	20	AA14043
11	19	79.2	219	21	AA14043

12	19	79.2	222	22	AA14043
13	19	79.2	303	22	AA14043
14	19	79.2	327	21	AA14043
15	19	79.2	377	21	AA14043
16	19	79.2	526	20	AA14043
17	19	79.2	963	17	AA14043
18	19	79.2	992	22	AA14043
19	19	79.2	1012	22	AA14043
20	19	79.2	11	15	AA14043
21	19	79.2	11	15	AA14043
22	19	79.2	11	15	AA14043
23	19	79.2	11	15	AA14043
24	19	79.2	11	15	AA14043
25	19	79.2	11	15	AA14043
26	19	79.2	11	15	AA14043
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29	19	79.2	11	15	AA14043
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32	19	79.2	11	15	AA14043
33	19	79.2	11	15	AA14043
34	19	79.2	11	15	AA14043
35	19	79.2	11	15	AA14043
36	19	79.2	11	15	AA14043
37	19	79.2	11	15	AA14043
38	19	79.2	11	15	AA14043
39	19	79.2	11	15	AA14043
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45	19	79.2	11	15	AA14043
46	19	79.2	11	15	AA14043
47	19	79.2	11	15	AA14043
48	19	79.2	11	15	AA14043
49	19	79.2	11	15	AA14043
50	19	79.2	11	15	AA14043

ALIGNMENTS

RESULT 1	AA1453	standard; Protein: 388 AA.
ID	AA1453	
AC	AA1453	
XX	22-OCT-2001	(first entry)
DT	22-OCT-2001	(first entry)
XX	22-OCT-2001	(first entry)
DE	Human polypeptide SEQ ID NO 6384.	
XX	Human; noctropic; immunosuppressant; cytosolic; gene therapy; cancer;	
KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukemia.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200153312-A1.	
PN	26-JUL-2001.	
XX	26-JUL-2001.	
PD	26-JUL-2001.	
XX	26-JUL-2001.	
XX	26-JUL-2001.	
PF	26-DEC-2000; 2000WO-US34263.	
XX	26-DEC-2000; 2000WO-US34263.	
PR	21-JAN-2000; 2000US-0488725.	
PR	25-APR-2000; 2000US-0552317.	
PR	09-JUL-2000; 2000US-0598042.	
PR	19-JUL-2000; 2000US-0620312.	

Human colon cancer
Human transferrin
Arabidopsis thaliana
Arabidopsis thaliana
S. erythraea PR137
Thermotoga maritima
Ephrin type-A receptor
Human kinase (PKIN)
Nucleoside anti-in
Anti-inflammatory p
Anti-inflammatory p
Human cell death p
Arabidopsis thaliana
Human colon cancer
Amino acid sequenc
WO9914235 Seq ID N
WO9914235 Seq ID N
Human secreted pro
Human secreted pro
Human protein sequ
Murine erythroid d
Amino acid sequenc
Arabidopsis thaliana
Polypeptide fragme
Human 5' EST seque
Arabidopsis thaliana
Porcine preprothrom
Molluscan receptor,
Pig molluscan. Sus
Kapost's sarcoma a
Human secreted pro
Arabidopsis thaliana

PR	03-ANG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSE-) HXSD INC.
PI	Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QH, Zhou P, Goodrich R, Dimanac RT;
XX	
DR	WFI: 2001-442253/47.
NR	N-Psdb: AA160609.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
PS	
XX	
XX	Example 2: SEQ ID NO 6384, 10078bp: English.
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC	immunosuppressant and cytosstatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neurophetic and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Draeger Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemia and
CC	C.N.S. disorders
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
SQ	
XX	Sequence 388 AA:
QY	
DB	131 laayrasl 138
XX	
DE	Query Match 83.3%; Score 20; DB 22; Length 388;
ID	Best Local Similarity 50.0%; Pred. No. 9.7e+02;
XX	Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX	
XX	1 LKXYRXL 8
XX	
XX	
XX	131 laayrasl 138
XX	
XX	Result 2
XX	AAM39667
XX	AAM39667 standard; Protein; 576 AA.
XX	
XX	AAM39667;
XX	
XX	22-OCT-2001 (first entry)
XX	
XX	Human polypeptide SEQ ID NO 2812.
XX	
KM	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM	peripheral nervous system; neuropathy; central nervous system; CNS;
KM	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM	amyotrophic lateral sclerosis; Shy-Draeger syndrome; chemotactic;
KM	chemokine; thrombolytic; drug screening; arthritis; inflammation;
KM	leukemia.
OS	Homo sapiens.
PN	WO200153312-A1.
PD	26-JUL-2001.
XX	
XX	26-DEC-2000; 2000MO-US34263.

PR	21-JAN-2000;	20000US-0488725.
PR	25-APR-2000;	20000US-055317.
PR	09-JUL-2000;	20000US-0596042.
PR	19-JUL-2000;	20000US-0620112.
PR	03-AUG-2000;	20000US-0653450.
PR	14-SEP-2000;	20000US-0661491.
PR	15-OCT-2000;	20000US-0693036.
PR	29-NOV-2000;	20000US-0727344.
XX		
XX	(HYSE-) HYSEQ INC.	
XX		
XX	Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
XX	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	
XX	Zhao QA, Zhou P, Goodrich R, Drmanac RT;	
XX		
XX	WPI: 2001-442253/47.	
DR	N-PSDB: AA158823.	
XX		
PT	Novel nucleic acids and polypeptides, useful for treating disorders	
PT	such as central nervous system injuries -	
XX		
XX	Example 4: SEQ ID NO 2812; 10078bp; English.	
XX		
CC	The invention relates to human nucleic acids (AA157798-AA161369) and	
CC	the encoded polypeptides (AA163647-AA1642213) with nootropic,	
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	localized neuropathies and central nervous system diseases, such as	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilization of the activities such as: Immune system suppression,	
CC	activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	
CC	assays for receptor activity, arthritis and inflammation, leukaemias and	
CC	C.N.S disorders.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification.	
XX		
XX	Sequence 576 AA:	
SO		
	Query Match 83.3%; Score 20; DB 22; Length 576;	
	Best local similarity 50.0%; Pred. No. 1.4e+03;	
	Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
OY	1 LXXYRXXL 8	
DB	319 laayraal 326	
RESULT 3		
XX	AA1614043	
XX	AA1614043 standard; Protein: 42 AA.	
XX	AA1614043;	
XX		
XX	12-OCT-2001 (first entry)	
DE	Peptide #477 encoded by probe for measuring cervical gene expression.	
XX	Probe: human; microarray; gene expression; cervical epithelial cell;	
XX	cervical cancer.	
XX		
XX	Hom sapiens.	
XX		
XX	WO200157278-A2.	
XX		
XX	09-AUG-2001.	
XX		
XX	30-JAN-2001; 2001WO-US00670.	
XX		

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:15:56 ; Search time 94.43 Seconds
(without alignments)
1.906 Million cell updates/sec

Title: US-09-281-760C-3
Perfect score: 24
Sequence: 1 LXXYRXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	19	79.2	526	2	US-08-852-401-3
2	19	79.2	963	1	US-08-537-002A-3
3	19	79.2	963	3	US-08-863-010-3
4	19	79.2	963	4	US-09-024-429-3
5	18	75.0	11	6	5177060-30
6	18	75.0	30	4	US-09-461-697-314
7	18	75.0	76	1	US-08-519-777-19
8	18	75.0	76	1	US-08-519-777-22
9	18	75.0	76	1	US-08-742-035-19
10	18	75.0	76	1	US-08-742-035-22
11	18	75.0	76	2	US-08-777-019-19
12	18	75.0	76	2	US-08-777-019-22
13	18	75.0	76	2	US-08-777-143-19
14	18	75.0	76	2	US-08-777-143-22
15	18	75.0	76	3	US-08-775-414-19
16	18	75.0	76	3	US-08-775-414-22
17	18	75.0	76	4	US-08-931-858E-19
18	18	75.0	76	4	US-08-931-858E-22
19	18	75.0	76	4	US-08-981-739-19
20	18	75.0	76	4	US-08-981-739-22
21	18	75.0	95	1	US-08-519-777-23
22	18	75.0	95	1	US-08-519-777-24
23	18	75.0	95	1	US-08-742-035-23
24	18	75.0	95	1	US-08-742-035-24
25	18	75.0	95	2	US-08-777-019-23
26	18	75.0	95	2	US-08-777-019-24
27	18	75.0	95	2	US-08-777-143-23

28	18	75.0	95	2	US-08-777-143-24	Sequence 24, Appl
29	18	75.0	95	3	US-08-775-414-23	Sequence 23, Appl
30	18	75.0	95	3	US-08-775-414-24	Sequence 24, Appl
31	18	75.0	95	4	US-08-931-858E-23	Sequence 23, Appl
32	18	75.0	95	4	US-08-931-858E-24	Sequence 24, Appl
33	18	75.0	95	4	US-08-981-739-23	Sequence 23, Appl
34	18	75.0	95	4	US-08-981-739-24	Sequence 24, Appl
35	18	75.0	119	4	US-09-046-479-4	Sequence 4, Appl
36	18	75.0	121	1	US-08-420-235B-23	Sequence 23, Appl
37	18	75.0	121	4	US-08-793-624-23	Sequence 23, Appl
38	18	75.0	121	5	PCT-US95-10194-82	Sequence 23, Appl
39	18	75.0	142	3	US-08-775-414-82	Sequence 82, Appl
40	18	75.0	144	3	US-08-775-414-81	Sequence 81, Appl
41	18	75.0	150	3	US-08-775-414-84	Sequence 84, Appl
42	18	75.0	152	3	US-08-775-414-83	Sequence 83, Appl
43	18	75.0	191	1	US-08-159-784-3	Sequence 8, Appl
44	18	75.0	195	1	US-08-519-777-8	Sequence 8, Appl
45	18	75.0	195	1	US-08-742-035-8	Sequence 8, Appl
46	18	75.0	195	2	US-08-777-143-8	Sequence 8, Appl
47	18	75.0	195	2	US-08-777-143-8	Sequence 8, Appl
48	18	75.0	195	3	US-08-775-414-8	Sequence 8, Appl
49	18	75.0	195	4	US-08-931-858E-8	Sequence 8, Appl
50	18	75.0	195	4	US-08-981-739-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-852-401-3
Sequence 3, Application US/08852401
Patent No. 5976836
GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
APPLICANT: Hessler, Paul E.
APPLICANT: Larsen, Peter E.
APPLICANT: Luu, B. Minh
TITLE OF INVENTION: Methods and Compositions for Enhancing
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockett, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,401
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa L.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: FER2159POO30US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-852-401-3

Query Match 79.2%; Score 19; DB 2; Length 526;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 LXXYRXL 8
Db 447 LSTYRXAL 454

RESULT 2
US-08-537-002A-3
Sequence 3, Application US/08537002A
Patent No. 5773282
GENERAL INFORMATION:
APPLICANT: TSUSAKI, Keiji
APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR
TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,002A
FILING DATE: 29-SEP-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 260984/1994
FILING DATE: 01-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP No. 5773282 yet received
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TSUSAKI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 963 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-537-002A-3

Query Match 79.2%; Score 19; DB 1; Length 963;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 LXXYRXL 8
Db 912 LQATRSAL 919

RESULT 3
US-08-863-010-3
Sequence 3, Application US/08863010

Patent No. 6087146
GENERAL INFORMATION:
APPLICANT: TSUSAKI, Keiji
APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR
TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,010
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/537,002
FILING DATE: 29-SEP-1995
APPLICATION NUMBER: JP 260984/1994
FILING DATE: 01-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP No. 6087146 yet received
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TSUSAKI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 963 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-863-010-3

Query Match 79.2%; Score 19; DB 3; Length 963;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 LXXYRXL 8
Db 912 LQATRSAL 919

RESULT 4
US-09-024-429-3
Sequence 3, Application US/09024429
Patent No. 6165768
GENERAL INFORMATION:
APPLICANT: TSUSAKI, Keiji
APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR
TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK
STREET: 419 Seventh Street, N.W., Suite 300

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:17:58 ; Search time 102.84 Seconds
(without alignments)
5.185 Million cell updates/sec

Title: US-09-281-760C-4
Sequence: 1 TLLEYRM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: pirl1:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	85.7	171	2	C86750
2	30	85.7	308	2	H65035
3	30	85.7	308	2	A85904
4	30	85.7	324	2	E70532
5	30	85.7	326	2	S72945
6	30	85.7	421	2	S38110
7	30	85.7	2368	2	S46005
8	29	82.9	267	2	T33911
9	29	82.9	315	2	T33910
10	29	82.9	344	2	T33909
11	29	82.9	388	2	T33908
12	29	82.9	531	2	T21059
13	29	82.9	631	2	C96768
14	29	82.9	988	2	A40628
15	28	82.9	2150	2	T08165
16	28	80.0	223	2	S48765
17	28	80.0	256	2	A69129
18	28	80.0	501	2	A29487
19	28	80.0	501	2	A34236
20	28	80.0	526	1	P5XR15
21	28	80.0	526	1	P5XR15
22	28	80.0	526	1	A45185
23	28	80.0	526	2	S18768
24	28	80.0	617	2	T23952
25	28	80.0	951	2	T41041
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27	27	77.1	214	2	C70865
28	27	77.1	214	2	C70865
29	27	77.1	216	2	D70813

30	27	77.1	246	1	G64166	heme export protei
31	27	77.1	265	2	T20127	hypothetical prote
32	27	77.1	353	2	A41558	N-syndecan - rat (
33	27	77.1	384	2	F82030	probable GTP-bind
34	27	77.1	384	2	D81007	GTP-binding protei
35	27	77.1	386	2	F82721	two-component syst
36	27	77.1	576	2	A84898	hypothetical prote
37	27	77.1	594	2	D71347	hypothetical prote
38	27	77.1	653	2	T47581	conserved hypothet
39	27	77.1	653	2	T51244	SCARECROW1 - Arabi
40	27	77.1	783	2	T38690	probable regulator
41	27	77.1	1160	2	T00272	hypothetical prote
42	26	74.3	82	2	I50968	MHC class II beta
43	26	74.3	82	2	I50984	MHC class II beta
44	26	74.3	82	2	I50986	MHC class II beta
45	26	74.3	237	2	T10629	hypothetical prote
46	26	74.3	255	2	S74068	hypothetical prote
47	26	74.3	282	2	JC7333	multicystatin - co
48	26	74.3	290	2	S50050	hypothetical prote
49	26	74.3	313	2	T23675	hypothetical prote
50	26	74.3	318	2	T02288	hypothetical prote

ALIGNMENTS

RESULT 1
C86750
hypothetical protein ykda [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: C86750
R:Boletun, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Gene Res. In press, 2001
A:Title: The complete genome sequence of the lactic acid bacterium.
A:Reference number: A86625
A:Accession: C86750
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <STC>
A:Cross-references: GB:AE005176; NID:g12723950; PIDN:AAK05101.1; GSPDB:GNC00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ykda

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 171;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLLEYR 6
|||||
DB 145 TLLEYR 150

RESULT 2
H65035
hypothetical protein srmb-ung intergenic region - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 17-Mar-2000
C:Accession: H65035
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H65035
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-308 <BLAT>
A:Cross-references: GB:AE000344; GB:U00096; NID:g1788927; PIDN:AACT5630.1; PID:g17889
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:

A:Gene: yf1e
C:Superfamily: Pseudomonas putida regulatory protein catr

Query Match 85.7%; Score 30; DB 2; Length 308;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLELYRM 7
|||||
DB 114 TLELYRM 120

RESULT 3

Probable transcription regulator lysR-type yf1e [Imported] - Escherichia coli (strain O1
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: A85904

R:Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimmlanta, E.; Potamocists, K.; Apodaca,
Mature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; PMID:21074935; PMID:11206551
A:Accession: A85904
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-308 <STO>
A:Cross-references: GB:AE005174; NID:q12516998; PIDN:AGS7693.1; GSPDB:GN00145; UWGP:Z38
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yf1e

Query Match 85.7%; Score 30; DB 2; Length 308;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLELYRM 7
|||||
DB 114 TLELYRM 120

RESULT 4

hypothetical protein RV2714 - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: E70532

R:Cole, S.T.; Brosch, R.; Parham, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, A.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; PMID:98295987
A:Accession: E70532
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-324 <COL>
A:Cross-references: GB:296072; GB:AL123456; NID:q3261793; PIDN:CAB09474.1; PID:q320946;
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: RV2714

Query Match 85.7%; Score 30; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LLELYRM 7
|||||
DB 194 LLELYRM 199

RESULT 5

hypothetical protein B2235_F1_6 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S72945

R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B2235.
A:Reference number: S72587
A:Accession: S72945
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <SMI>
A:Cross-references: EMBL:U00019; NID:q467079; PIDN:AA17281.1; PID:q4670798

Query Match 85.7%; Score 30; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LLELYRM 7
|||||
DB 196 LLELYRM 201

RESULT 6

O-sialoglycoprotein endopeptidase homolog YKR038c - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 11-Jan-2000
C:Accession: S38110
R:Rustera, L.A.; Jauniaux, J.C.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S38097
A:Accession: S38110
A:Molecule type: DNA
A:Residues: 1-421 <UNP>
A:Cross-references: EMBL:Z28263; NID:q486476; PID:q486477; MIPS:YKR038c
C:Genetics:
A:Map position: 11R
C:Superfamily: O-sialoglycoprotein endopeptidase
C:Keywords: calcium binding; EF hand
F:271-283/Domain: calcium binding #status predicted <CAI>

Query Match 85.7%; Score 30; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LLELYRM 7
|||||
DB 389 LLELYRM 394

RESULT 7

ESR1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: MEC1 protein; protein YBR1012; protein YBR136w
C:Species: Saccharomyces cerevisiae
C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 29-Oct-1999
C:Accession: S46005; S46578; S46663; S47954; S64650
R:Beck, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S46005
A:Accession: S46005
A:Molecule type: DNA
A:Residues: 1-2368 <BEC>
A:Cross-references: EMBL:Z36005; NID:q536429; PIDN:CAA85094.1; PID:q536430; MIPS:YBR1
A:Experimental source: strain S288C

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:37:25 ; Search time 85.5 Seconds
(without alignments)
3.002 Million cell updates/sec

Title: US-09-281-760C-4
Perfect score: 35
Sequence: 1 TLLEYRM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Imm DB seq length: 0
Imm DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match Length	ID	Description
1	30	85.7	293 1 YFIE_ECOLI	P3634 escherichia
2	30	85.7	421 1 YK18_YEAST	P36132 saccharomyc
3	30	85.7	2368 1 ESR1_YEAST	P38111 saccharomyc
4	29	82.9	589 1 L01A_LYCPN	O04973 lycopersico
5	29	82.9	612 1 L01B_LYCPN	O04974 lycopersico
6	29	82.9	988 1 TNP6_ENTFC	O06238 enterococcu
7	28	80.0	223 1 YD78_YEAST	P38957 saccharomyc
8	28	80.0	432 1 GBA1_CRYNE	P54853 cryptococcu
9	28	80.0	501 1 CP36_RABIT	P11707 cytochrome
10	28	80.0	526 1 VP5_BTVIA	P12436 bluetongue
11	28	80.0	526 1 VP5_BTVIA	P12436 bluetongue
12	28	80.0	526 1 VP5_BTVIA	P12436 bluetongue
13	28	80.0	526 1 VP5_BTVIA	P12436 bluetongue
14	27	77.1	214 1 CLP2_MYCTU	O9cb47 mycobacteri
15	27	77.1	214 1 CLP2_MYCTU	O9cb47 mycobacteri
16	27	77.1	246 1 CMC_HAEIN	P45034 haemophilus
17	27	77.1	384 1 SDC3_HUMAN	O75056 homo sapien
18	27	77.1	433 1 Y681_PASMU	P57864 pasteurella
19	27	77.1	442 1 SDC3_MOUSE	O64519 mus musculu
20	27	77.1	442 1 SDC3_MOUSE	O64519 mus musculu
21	27	77.1	1160 1 WDR7_HUMAN	O9y466 homo sapien
22	26	74.3	213 1 RL3_STYP6	O24689 synecococc
23	26	74.3	436 1 CG2B_DICD1	P42524 dictyosteli
24	26	74.3	505 1 SYE_CHLPN	O92753 chlamydia p
25	26	74.3	508 1 ATPD_MAIZE	P05444 zea mays (m
26	26	74.3	508 1 ATPD_MAIZE	P05444 zea mays (m
27	26	74.3	509 1 ATPD_ORXSA	P15998 oryza sativ
28	26	74.3	509 1 ATPD_ORXSA	P15998 oryza sativ
29	26	74.3	741 1 TAX4_CABEL	O03611 caenorhabdi
30	26	74.3	741 1 TAX4_CABEL	O03611 caenorhabdi
31	26	74.3	856 1 CLPB_HAEIN	P44403 haemophilus
32	26	74.3	859 1 LOX1_ARATH	O06327 arabidopsis
33	26	74.3	962 1 YAAE_SCHPO	O09731 schizosacch

ALIGNMENTS

RESULT	ID	STANDARD	PRT	293 AA.
YFIE_ECOLI	AC	P3634; P76592; P76998;		
YFIE_ECOLI	DT	01-FEB-1994 (Rel. 28, Created)		
YFIE_ECOLI	DT	01-NOV-1997 (Rel. 35, Last sequence update)		
YFIE_ECOLI	DT	20-AUG-2001 (Rel. 40, Last annotation update)		
YFIE_ECOLI	DE	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR YFIE.		
YFIE_ECOLI	GN	YFIE OR P2577.		
YFIE_ECOLI	OS	Escherichia coli.		
YFIE_ECOLI	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
YFIE_ECOLI	OC	Escherichia.		
YFIE_ECOLI	OX	NCBI_TaxID=562;		
YFIE_ECOLI	OX	NCBI_TaxID=562;		
YFIE_ECOLI	RP	SEQUENCE FROM N.A.		
YFIE_ECOLI	RP	STRAIN-K12;		
YFIE_ECOLI	RA	Nashimoto H.;		
YFIE_ECOLI	RT	"Non-ribosomal proteins affecting the assembly of ribosomes in		
YFIE_ECOLI	RT	Escherichia coli.";		
YFIE_ECOLI	RL	(In) Niehaus K.H. (eds.);		
YFIE_ECOLI	RL	The translational apparatus, pp.165-195, Plenum Press,		
YFIE_ECOLI	RL	New York (1993).		
YFIE_ECOLI	RL	[2]		
YFIE_ECOLI	RP	SEQUENCE FROM N.A.		
YFIE_ECOLI	RP	STRAIN-K12;		
YFIE_ECOLI	RA	Nashimoto H., Saito N.;		
YFIE_ECOLI	RT	Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.		
YFIE_ECOLI	RL	[3]		
YFIE_ECOLI	RP	SEQUENCE FROM N.A.		
YFIE_ECOLI	RP	STRAIN-K12 / MG1655;		
YFIE_ECOLI	RC	MEDLINE-97426617; PubMed-9278503;		
YFIE_ECOLI	RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,		
YFIE_ECOLI	RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,		
YFIE_ECOLI	RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,		
YFIE_ECOLI	RA	Ma B., Shao Y.;		
YFIE_ECOLI	RT	"The complete genome sequence of Escherichia coli K-12.";		
YFIE_ECOLI	RT	Science 277:1453-1474(1997).		
YFIE_ECOLI	RL	[4]		
YFIE_ECOLI	RP	SEQUENCE OF 1-208 FROM N.A.		
YFIE_ECOLI	RC	STRAIN-K12.		
YFIE_ECOLI	RC	MEDLINE-97349980; PubMed-9205837;		
YFIE_ECOLI	RA	Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,		
YFIE_ECOLI	RA	Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,		
YFIE_ECOLI	RA	Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,		
YFIE_ECOLI	RA	Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubraman S.,		
YFIE_ECOLI	RA	Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,		
YFIE_ECOLI	RA	Yamagata S., Horiiuchi T.;		
YFIE_ECOLI	RT	"Construction of a contiguous 874-kb sequence of the Escherichia coli		
YFIE_ECOLI	RT	- K12 genome corresponding to 50.0-68.8 min on the linkage map and		
YFIE_ECOLI	RT	analysis of its sequence features.";		
YFIE_ECOLI	RT	DNA Res. 4:91-113(1997).		

34	26	74.3	1362 1 CA21_CHICK	P02467 gallus gall
35	26	74.3	1595 1 SOS_DROME	P26675 drosophila
36	25	71.4	29 1 HS98_NEUCR	P31540 neuropepta
37	25	71.4	82 1 VPV_HV1BN	P12516 human immun
38	25	71.4	111 1 RL29_MYCPN	O50310 mycoplasma
39	25	71.4	153 1 RL29_MYCPN	O52340 mycoplasma
40	25	71.4	183 1 IMP3_YEAST	P32899 saccharomyc
41	25	71.4	195 1 Y188_BACHD	O9kb07 bacillus ha
42	25	71.4	200 1 RL29_MYCPN	P47405 mycoplasma
43	25	71.4	208 1 EFH1_TRYCR	P41049 trypanosoma
44	25	71.4	208 1 EFH1_TRYCR	P41049 trypanosoma
45	25	71.4	211 1 YL71_ARCRU	O28111 archaeoglob
46	25	71.4	214 1 Y023_CABEL	P34673 caenorhabdi
47	25	71.4	226 1 ATP6_BALMO	P41291 dalaenopter
48	25	71.4	227 1 MTR2_MOUSE	O9y4x7 aeropyrum p
49	25	71.4	234 1 AOX2_AERPE	O9y4x7 aeropyrum p
50	25	71.4	238 1 VSP1_AGRHA	P81176 agkistrodon

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CC -----
CC EMBL: D13169; -; NOT_ANNOTATED_CDS.
CC EMBL: D64044; -; NOT_ANNOTATED_CDS.
CC EMBL: AE000344; AAC75630.1; ALT_INTT.
CC EMBL: D90886; BAA20920.1; -.
CC Ecogene; EG11785; YFE.
CC InterPro: IPR000847; HTH_LysR.
CC Pfam: PF00126; HTH_1; 1.
CC PROSITE: PS00044; HTH_LYSR_FAMILY; 1.
CC Hypothetical protein; Transcription regulation; DNA-binding;
CC Complete proteome.
CC DNL_BIND 18 37 H-T-H MOTIF (BY SIMILARITY).
CC CONFLICT 209 293 RITVENTELISIKRCVANNIGSVLPPRAAKELEG
CC ELIELPGEOSITSMCAHHKRAVSPAMHTFCVEESF
CC VAG -> DHGCKH (IN REF. 1 AND 2).
CC -----
CC QUERY MATCH 293 AA: 33243 MW: 105496647799632 CRC64:
CC Best Local Similarity 85.7%; Score 30; DB 1; Length 293;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 TLEFRM 7
CC 99 TLEFRM 105
CC -----
CC RESULT 2
CC YK18_YEAST STANDARD; PRT; 421 AA.
CC AC P36132;
CC DT 01-JUN-1994 (Rel. 29, Created)
CC DT 01-JUN-1994 (Rel. 29, Last sequence update)
CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
CC DE HYPOHETICAL 46.6 KDA PROTEIN IN DAL80-GAP1 INTERGENIC REGION.
CC GN YKR038C.
CC OS Saccharomyces cerevisiae (Baker's yeast).
CC NC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC NC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CC NCBI_TaxId=4932;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA Urrestarazu L.A.; Juniaux J.-C.;
CC RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COULD BE A METALLOPROTEASE.
CC -1- CORONATOR: ZINC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M22. ALSO KNOWN AS THE
CC GLYCOPROTEASE FAMILY.
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CC -----
CC EMBL: Z28263; CAA82112.1; -.
CC EMBL: P38110; S38110.
CC SGD: S0001746; YKR038C.
CC InterPro: IPR000905; Peptidase_M22.
CC Pfam: PF00814; Peptidase_M22; 1.
CC DR PRINTS: PR00789; OSIALOPEASE.

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CC DR PRODOM: PD002367; Peptidase_M22; 1.
CC DR PROSITE: PS01016; GLYCOPROTEASE; 1.
CC KW Hypothetical protein; Hydrolase; Metalloprotease; Zinc.
CC FT METAL 176 176 ZINC (POTENTIAL).
CC FT METAL 180 180 ZINC (POTENTIAL).
CC SEQUENCE 421 AA: 46602 MW: 05721149822277F CRC64:
CC -----
CC QUERY MATCH 85.7%; Score 30; DB 1; Length 421;
CC Best Local Similarity 100.0%; Pred. No. 16;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 2 LLEFRM 7
CC 389 LLEFRM 394
CC -----
CC RESULT 3
CC ESRL_YEAST STANDARD; PRT; 2368 AA.
CC ID ESRL_YEAST
CC AC P38111; Q02580;
CC DT 01-OCT-1994 (Rel. 30, Created)
CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
CC DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC DE ESRL PROTEIN.
CC GN ESRL OR MECL OR SAD3 OR YBR136V OR YBR1012.
CC OS Saccharomyces cerevisiae (Baker's yeast).
CC NC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC NC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CC NCBI_TaxId=4932;
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA MEDLINE-9434472; PubMed-8065923;
CC RX Kato R., Ogawa H.;
CC RT "An essential gene, ESRL, is required for mitotic cell growth, DNA
CC RT repair and meiotic recombination in Saccharomyces cerevisiae.";
CC RL Nucleic Acids Res. 22:3104-3112(1994).
CC [2]
CC RP SEQUENCE FROM N.A.
CC RA Weiner T.A., Harlow D.;
CC RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC [3]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-S288C;
CC RX MEDLINE-94378717; PubMed-8091856;
CC RA Becam A.-M., Cullin C., Gryzboska E., Lacroix F., Nasr F.,
CC RA Orliez-Kalogreopoulos O., Palucha A., Slonimski P.P., Zagulski M.,
CC RA Herbert C.J.;
CC RT "The sequence of 29.7 kb from the right arm of chromosome II reveals
CC RT 13 complete open reading frames, of which ten correspond to new
CC RT genes."
CC RL Yeast 10:S1-S11(1994).
CC -1- FUNCTION: REQUIRED FOR CELL GROWTH, DNA REPAIR AND MEIOTIC
CC -1- RECOMBINATION.
CC -1- DEVELOPMENTAL STAGE: INDUCED DURING MEIOSIS.
CC -1- SIMILARITY: IN THE N-TERMINAL REGION, TO S.POMBE CDT1.
CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.
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CC -----
CC EMBL: X75891; CAA53494.1; -.
CC EMBL: U31109; AAA74482.1; -.
CC EMBL: Z36005; CAA95094.1; -.
CC EMBL: D11088; BAA01860.1; -.
CC PIR: S46005; S46005.
CC PIR: S46378; S46378.
CC SGD: S0000340; MECL.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:35:50 ; Search time 191.29 Seconds

(without alignments)
5.353 Million cell updates/sec

Title: US-09-281-760c-4

Sequence: 1 TITLE: 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :

1: SPREMBL_17:*
2: SP_Archaea:*
3: SP_Fungi:*
4: SP_Human:*
5: SP_Invertebrate:*
6: SP_Mammal:*
7: SP_mhc:*
8: SP_Organelle:*
9: SP_Phage:*
10: SP_Plant:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	85.7	171	2	09JN51
2	30	85.7	171	2	09CGR9
3	30	85.7	324	2	007213
4	30	85.7	326	2	049847
5	30	85.7	330	2	09CPB9
6	30	85.7	422	2	09LCY8
7	29	82.9	267	5	09TYL5
8	29	82.9	315	5	09TYL6
9	29	82.9	344	5	09TYL7
10	29	82.9	388	5	09TYL8
11	29	82.9	531	5	019518
12	29	82.9	631	10	09C550
13	29	82.9	675	10	09LPR4
14	29	82.9	2150	12	037086
15	28	80.0	236	1	026335
16	28	80.0	565	2	09REN5
17	28	80.0	587	4	095876
18	28	80.0	617	5	09U398
19	28	80.0	851	3	094418

20	28	80.0	919	1	09YF21	09Yf21 aeropyrum p
21	27	77.1	126	2	086327	086327 mycobacteri
22	27	77.1	216	2	053856	053856 mycobacteri
23	27	77.1	233	2	09RB41	09rb41 cytophaga j
24	27	77.1	247	10	041171	041171 rhodella vi
25	27	77.1	265	5	018763	018763 caenorhabdi
26	27	77.1	359	13	091BF8	091bf8 oryzias lat
27	27	77.1	378	2	091433	091433 xanthomonas
28	27	77.1	382	13	09DG99	09dg99 oryzias jav
29	27	77.1	384	2	09JXE5	09jxe5 neisseria m
30	27	77.1	384	2	09JWJ4	09jwj4 neisseria m
31	27	77.1	386	2	09PEB5	09peb5 xyella fas
32	27	77.1	386	13	09DG96	09dg96 oryzias luz
33	27	77.1	387	13	091BG0	091bg0 oryzias lat
34	27	77.1	388	13	09DGA3	09dga3 oryzias cur
35	27	77.1	409	8	09MR88	09mr88 euglypha ro
36	27	77.1	419	2	09RMU6	09rmu6 helicobacte
37	27	77.1	453	5	09NKR8	09nkr8 drosophila
38	27	77.1	481	5	09VJW8	09vjw8 drosophila
39	27	77.1	530	5	09GPF0	09gpf0 dictyostell
40	27	77.1	576	5	09W329	09w329 drosophila
41	27	77.1	576	10	082364	082364 arabidopsis
42	27	77.1	594	2	083287	083287 treponema p
43	27	77.1	653	10	096304	096304 arabidopsis
44	27	77.1	653	10	09M384	09m384 arabidopsis
45	27	77.1	762	5	09UZF2	09ufz2 caenorhabdi
46	27	77.1	774	2	P95636	P95636 rhodospheo
47	27	77.1	783	3	014130	014130 schizosacch
48	27	77.1	853	4	09BS12	09bs12 homo sapien
49	27	77.1	1024	2	099XQ8	099xq8 streptococc
50	27	77.1	1488	11	09ERN3	09ern3 rattus norv

ALIGNMENTS

RESULT 1
ID 09JN51 PRELIMINARY; PRT; 171 AA.
AC 09JN51;
DT 01-OCR-2000 (TRENBLREL. 15, Created)
DT 01-OCR-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCR-2000 (TRENBLREL. 15, Last annotation update)
DE TCSORF2.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MG1363;
RX MEDLINE=97316457; PubMed=9172368;
RA O'Connell-Motherway M., Fitzgerald G.F., van Sinderen D.;
RT "Cloning and sequence analysis of putative histidine protein kinases
isolated from Lactococcus lactis MG1363.";
RT Appl. Environ. Microbiol. 63:2454-2459(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MG1363;
RX MEDLINE=20244638; PubMed=10784052;
RA O'Connell-Motherway M., van Sinderen D., Morel-Deville F.,
Fitzgerald G.F., Enrich S.D., Morel P.;
RT "Six putative two-component regulatory systems isolated from
Lactococcus lactis subsp. cremoris MG1363.";
RL Microbiology 146:935-947(2000).
DR EMBL: U81488; AAF6143.1; -;
SQ SEQUENCE 171 AA; 19171 MW; 3D16FAD7BFF83819 CXC64;

Query Match 85.7%; Score 30; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TLEVR 6
Db 145 TLEVR 150

RESULT 2
O9CGT9 PRELIMINARY: PRT: 171 AA.
AC O9CGT9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
GN UNKNOWN PROTEIN.
YKDA.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
CX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1L1403;
RA Bolotin A., Mincker P., Manger S., Jallion O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis."
RL Genome Res. 0:0-0(2001).
DR EMBL; AE006334; AAK05101.1; -.
KW Complete proteome.
SQ SEQUENCE 171 AA; 19216 MW; 975EEFBC50329BF9 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLEVR 6
Db 145 TLEVR 150

RESULT 3
O07213 PRELIMINARY: PRT: 324 AA.
ID O07213;
AC 007213;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
GN HYPOTHETICAL 35.5 KDA PROTEIN.
EN RV2714 OR MTCY05A6.35.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
DR EMBL; 296072; CAB09474.1; -.
KW Tuberculosis; RV2714; -.
SQ SEQUENCE 324 AA; 35519 MW; 45E4809917AB22B CRC64;

Query Match 85.7%; Score 30; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLEVR 6
Db 145 TLEVR 150

RESULT 4
O49847 PRELIMINARY: PRT: 326 AA.
ID O49847;
AC O49847;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE B2235_F1_6 (HYPOTHETICAL PROTEIN ML1009).
GN ML1009.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=JN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Fellwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrett B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 409:1007-1011(2001).
DR EMBL; U00019; AAA17281.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 326 AA; 36152 MW; D089CF228598C722 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TLEVR 7
Db 196 TLEVR 201

RESULT 5
O9CPB9 PRELIMINARY: PRT: 330 AA.
ID O9CPB9;
AC O9CPB9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FECD.
SQ SEQUENCE 330 AA; 35519 MW; 45E4809917AB22B CRC64;
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:14:10 ; Search time 158.02 Seconds
(without alignments)
3.281 Million cell updates/sec

Title:	US-09-281-760C-4
Perfect score:	35
Sequence:	1 TLLEYRM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 522463
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Maximum DB seq length: 0
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	50 summaries

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21:	/SIDSL/gcgdata/geneseq/geneseqp/AA2001.DAT *
22:	/SIDSL/gcgdata/geneseq/geneseqp/AA2002.DAT *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	35	100.0	7	21	AAV6584
2	35	100.0	7	21	AAV50878
3	30	85.7	421	21	AAV59253
4	30	85.7	2368	18	AAW26663
5	30	85.7	2368	20	AAW73893
6	29	82.9	545	20	AAV26187
7	29	82.9	988	13	AAR24302
8	28	80.0	135	20	AAV41237
9	28	80.0	304	22	AAB93395
10	28	80.0	554	22	AAB94147
11	27	77.1	10	20	AAV45789

12	27	77.1	11	7	AAP60980	Polypeptide which
13	27	77.1	38	21	AAB58532	lung cancer associ
14	27	77.1	44	22	AAAM18108	Peptide #4632 enco
15	27	77.1	53	21	AAAB43458	Human cancer assoc
16	27	77.1	78	22	AAAM57911	Peptide #11948 enc
17	27	77.1	89	22	AAAM18904	Peptide #5338 enco
18	27	77.1	89	22	AAAM1445	Peptide #5482 enco
19	27	77.1	653	18	AAAB38178	Arbidopsis SCAREC
20	27	77.1	653	21	AAAB28559	Arbidopsis SCAREC
21	27	77.1	807	22	AAAM0412	Human polypeptide
22	27	77.1	1739	22	AAAM42197	Human polypeptide
23	26	74.3	157	21	AAAB6238	Human secreted pro
24	26	74.3	272	21	AAAG10183	Arbidopsis thaliaa
25	26	74.3	272	21	AAAG40522	Arbidopsis thaliaa
26	26	74.3	272	21	AAAT74877	Neisseria meningit
27	26	74.3	279	21	AAAG10182	Arbidopsis thaliaa
28	26	74.3	279	21	AAAG40521	Arbidopsis thaliaa
29	26	74.3	292	22	AAAG2082	C glutamicum prote
30	26	74.3	292	22	AAAB79400	Corynebacterium gl
31	26	74.3	295	22	AAAB79401	Corynebacterium gl
32	26	74.3	358	21	AAAG10181	Arbidopsis thaliaa
33	26	74.3	363	22	AAAG91536	C glutamicum prote
34	26	74.3	363	22	AAAB79069	Corynebacterium gl
35	26	74.3	386	21	AAAG40520	Arbidopsis thaliaa
36	26	74.3	515	20	AAAY35180	C. pneumoniae prot
37	26	74.3	589	22	AAAB95645	Human protein sequ
38	26	74.3	686	21	AAAG39711	Arbidopsis thaliaa
39	26	74.3	841	21	AAAB18511	H2 homologue of pr
40	26	74.3	915	20	AAAY34977	C. pneumoniae prot
41	26	74.3	924	22	AAAB93084	Human protein sequ
42	26	74.3	924	22	AAAB95845	Human protein sequ
43	26	74.3	1596	21	AAAY68821	Amino acid sequenc
44	26	74.3	1876	22	AAAM58757	Phosphatidy l inosi
45	25	71.4	23	18	AAAU00611	VH ligand-binding
46	25	71.4	37	21	AAAB44726	Human secreted pro
47	25	71.4	67	21	AAAG08015	Arbidopsis thaliaa
48	25	71.4	96	21	AAAG08014	Arbidopsis thaliaa
49	25	71.4	103	22	AAAB61578	Polynavirus protei
50	25	71.4	123	18	AAAM11784	Early onset Alzhei

ALIGNMENTS

RESULT	1
AAV69584	
ID	AAV69584 standard; peptide; 7 AA.

AC AAY69584

DT 19-APR-2000 (first entry)

DE Immunogenic peptide SEQ ID NO:9, for anti-IgE autoantibody generation.

KW Immunogenic; autoimmunity; IgE autoantibody; immunoglobulin E;

KW allergy; canine; prophylaxis; treatment.

OS Synthetic.

PN EP955311-A2.

PD 10-NOV-1999.

PF 09-APR-1999; 99EP-0107020.

PR 09-APR-1998; 98US-0058332.

PR 30-MAR-1999; 99US-0281761.

PA (IDEX-) IDEXX LAB INC.

PI Lawton R, Mermer B, Francoeur G;

DR WPI; 2000-118182/11.

XX New peptides, useful for generating canine autoantibodies against
PT Immunoglobulin E (IgE) to treat allergic symptoms -
XX Claim 5, Page 5, 38pp; English.
XX Sequences AAY69576-Y69586 and AAY69598-Y69599 represent peptides that may
CC be used to induce anti-IgE (Immunoglobulin E) autoantibodies in a dog.
CC IgE is an important mediator of canine allergic responses, including Type
CC I immediate hypersensitivity. It is estimated that up to 30% of all dogs
CC suffer from allergies or allergy-related skin disorders, and allergic
CC dermatitis is thought to affect between 3 and 15% of dogs. Common canine
CC allergens include fleas, pollens, moulds and dust, with flea allergy
CC being the most frequent. Once IgE has been released in response to
CC allergen, the IgE binds to receptors on mast cells. The IgE molecules
CC can then become cross-linked, which induces the mast cells to release
CC histamine, which leads to the manifestation of allergic symptoms. The
CC peptides of the invention correspond to epitopes of canine IgE, or
CC conservative variations thereof that are accessible in circulating IgE
CC but not in IgE bound to mast cells. The autoantibodies produced on
CC immunisation with such peptides therefore target only circulating IgE,
CC avoiding the possibility that they may cross-link bound IgE molecules,
CC which would exacerbate an ongoing allergic response even in the absence
CC of allergen. Anti-IgE autoantibody induction results in an immune
CC response that targets the IgE-expressing B cell, which affects IgE
CC synthesis by downregulating IgE production by B cells and/or targeting
CC the IgE-producing B cell for destruction. The peptides of the invention
CC are therefore useful for the treatment or prophylaxis of allergic
CC symptoms in a dog.
XX Sequence 7 AA:
SQ
Query Match 100.0%; Score 35; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TLLETRM 7
Db 1 lileyrm 7
RESULT 2
ID AAY50878 standard; peptide; 7 AA.
XX AAY50878;
XX 24-FEB-2000 (first entry)
XX Antobody 8H.8 binding mimotope 1.
XX Canine; allergy; antobody 8H.8; IgE; B cell; mast cell; anti-allergy;
XX epitope; prophylaxis; treatment; mimotope.
XX Synthetic.
XX EP957111-A2.
XX 17-NOV-1999.
XX 09-APR-1999; 99EP-0107035.
XX 09-APR-1999; 98US-0058331.
XX 30-MAR-1999; 98US-0281760.
XX (IDEX-) IDEXX LAB INC.
XX Lawton R, Mermer B, Francoeur G;
XX WPI; 2000-040833/04.
XX Binding proteins used for treatment or prophylaxis of canine allergy -
PT

XX Claim 9, Page 12; 30pp; English.
XX This invention describes a novel binding protein which specifically
CC binds to native canine free or B-cell bound IgE, and which doesn't bind
CC to IgE when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy.
CC AAY50876-Y50900 represent peptide mimotopes used in the method of the
CC invention.
XX Sequence 7 AA:
SQ
Query Match 100.0%; Score 35; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TLLETRM 7
Db 1 lileyrm 7
RESULT 3
ID AAY59253 standard; Protein; 421 AA.
XX AAY59253;
XX 25-APR-2000 (first entry)
XX Yeast glycoprotease-like protein.
XX Glycoprotease; glycoprotease-like protein; cell proliferation; human;
XX immunosuppressant; immunosuppressant; thrombotic agent; tissue growth;
XX KW contraindicative; fertility-promoting agent; hematopoiesis; antimicrobial;
XX anti-inflammatory; anti-tumour; gene therapy; yeast.
XX Saccharomyces cerevisiae.
XX W09967399-A1.
XX 29-DEC-1999.
XX 24-JUN-1999; 99WO-JP03358.
XX 25-JUN-1998; 98JP-0178247.
XX (SAGA) SAGAMI CHEM RES CENT.
XX (PROT-) PROTEGENE INC.
XX Kato S, Kimura T;
XX WPI; 2000-147211/13.
XX A human protein with glycoprotease-like activity, used for diagnosis,
XX treatment and prevention of e.g. autoimmune disease or cancer -
XX Disclosure; Page 35; 55pp; English.
XX The invention provides a new human protein with glycoprotease activity.
XX The protein can be expressed by standard recombinant methodology. The
XX glycoprotease-like protein can be used to screen for specific-binding
XX agents (receptors or ligands) or inhibitors or agonists of its binding
XX interactions; to raise antibodies or elicit an immune response; as a
XX tissue marker; as a nutrient source or supplement; as a research reagent;
XX and as a therapeutic/biologically active agent, e.g. for regulating
XX cell proliferation or differentiation; as immunosuppressant or
XX immunosuppressant; as thrombotic agent; for stimulation of tissue
XX growth; as contraceptive/fertility-promoting agent; in regulation of
CC

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:15:57 ; Search time 94.43 Seconds
(without alignments)
1.668 Million cell updates/sec

Title: US-09-281-760C-4
Perfect score: 35
Sequence: 1 TLEFYM 7

Scoring table: BLOSUM62
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Searched: 212252 seqs, 22503292 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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6: /cgn2_6/prodata/1/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	85.7	2368	1	US-08-198-446B-15	Sequence 15, Appl
2	30	85.7	2368	2	US-08-870-693-15	Sequence 15, Appl
3	29	82.9	988	2	US-08-286-819A-19	Sequence 19, Appl
4	29	82.9	988	3	US-08-980-357-19	Sequence 19, Appl
5	28	80.0	135	3	US-09-053-197A-32	Sequence 32, Appl
6	27	77.1	1023	1	US-08-198-446B-4	Sequence 4, Appl
7	27	77.1	1023	2	US-08-870-693-4	Sequence 4, Appl
8	26	74.3	137	2	US-08-609-049A-14	Sequence 14, Appl
9	26	74.3	137	4	US-09-170-996-14	Sequence 14, Appl
10	26	74.3	430	2	US-08-290-731C-9	Sequence 9, Appl
11	26	74.3	1572	2	US-08-290-731C-5	Sequence 5, Appl
12	26	74.3	1596	3	US-09-356-952-3	Sequence 3, Appl
13	26	74.3	1876	2	US-08-609-049A-12	Sequence 12, Appl
14	26	74.3	1876	2	US-08-609-049A-28	Sequence 28, Appl
15	26	74.3	1876	4	US-09-170-996-12	Sequence 12, Appl
16	26	74.3	1876	4	US-09-170-996-28	Sequence 28, Appl
17	25	71.4	302	2	US-09-031-485-38	Sequence 38, Appl
18	25	71.4	302	2	US-08-847-429A-38	Sequence 38, Appl
19	25	71.4	302	3	US-09-065-474-38	Sequence 38, Appl
20	25	71.4	567	3	US-08-813-150-4	Sequence 4, Appl
21	25	71.4	690	2	US-08-619-554-8	Sequence 8, Appl
22	25	71.4	885	1	US-08-372-892-4	Sequence 4, Appl
23	25	71.4	888	1	US-08-445-640-35	Sequence 35, Appl
24	25	71.4	888	1	US-08-170-558-35	Sequence 35, Appl
25	25	71.4	888	3	US-08-447-314-35	Sequence 35, Appl
26	25	71.4	888	3	US-08-445-461-35	Sequence 35, Appl
27	25	71.4	892	1	US-07-977-434-12	Sequence 12, Appl

28	25	71.4	892	1	US-08-458-819-12	Sequence 12, Appl
29	25	71.4	892	5	PCT-US91-07035-12	Sequence 12, Appl
30	25	71.4	894	1	US-08-372-892-2	Sequence 2, Appl
31	25	71.4	894	1	US-08-445-640-34	Sequence 34, Appl
32	25	71.4	894	3	US-08-170-558-34	Sequence 34, Appl
33	25	71.4	894	3	US-08-447-314-34	Sequence 34, Appl
34	25	71.4	894	3	US-08-445-461-34	Sequence 34, Appl
35	25	71.4	1088	4	US-09-082-059-2	Sequence 2, Appl
36	25	71.4	1122	2	US-08-619-198-3	Sequence 3, Appl
37	25	71.4	1389	2	US-08-619-198-5	Sequence 5, Appl
38	25	71.4	1418	3	US-08-963-825-20	Sequence 20, Appl
39	25	71.4	1418	4	US-09-010-999-1	Sequence 1, Appl
40	25	71.4	1442	2	US-08-316-650-12	Sequence 12, Appl
41	25	71.4	1442	2	PCT-US95-02251-12	Sequence 12, Appl
42	25	71.4	1876	2	US-08-619-554-2	Sequence 2, Appl
43	25	71.4	1895	2	US-08-619-554-4	Sequence 4, Appl
44	24	68.6	28	1	US-07-977-630-48	Sequence 48, Appl
45	24	68.6	264	3	US-09-053-197A-8	Sequence 8, Appl
46	24	68.6	346	4	US-08-915-498B-27	Sequence 27, Appl
47	24	68.6	451	2	US-08-372-652-2	Sequence 2, Appl
48	24	68.6	451	5	PCT-US95-16311-2	Sequence 2, Appl
49	24	68.6	469	3	US-08-372-183-2	Sequence 2, Appl
50	24	68.6	469	4	US-09-469-721-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-198-446B-15
; Sequence 15, Application US/08198446B
; Patent No. 5674996
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Pion, Sharon E.
; APPLICANT: Groudine, Mark T.
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/198,446B
; FILING DATE: 18-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCRI7537
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2368 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Yeast Mccl protein
; US-08-198-446B-15
Query Match 85.7% ; Score 30; DB 1; Length 2368;

Best Local Similarity: 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLEVRM 7
1:1:111
DB 1647 TILDYRM 1653

RESULT 2
US-08-870-693-15
Sequence 15 Application US/08870693
Patent No. 5666338
GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Pion, Sharon E.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,446
FILING DATE: February 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: May 12, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Shelness, Diana K.
REGISTRATION NUMBER: 35,356
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
TELEFAX: 206-224-0779
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Yeast Mcc1 protein
US-08-870-693-15

Query Match 85.7%; Score 30; DB 2; Length 2368;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLEVRM 7
1:1:111
DB 1647 TILDYRM 1653

RESULT 3
US-08-286-819A-19
Sequence 19, Application US/08286819A

Patent No. 5871910
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPROTEIN IN PARTICULAR
TITLE OF INVENTION: INTRAMEMBRANE PROTEIN, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 988 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-286-819A-19

Query Match 82.9%; Score 29; DB 2; Length 988;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLEVRM 7
1:1:111
DB 120 TLEVRM 126

RESULT 4
US-08-980-357-19
Sequence 19, Application US/08980357
Patent No. 6013508

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:18:00 ; Search time 102.84 Seconds
(without alignments)
8.148 Million cell updates/sec

Title: US-09-281-760c-5
Perfect score: 63
Sequence: 1 GNMUTWRESK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Immum DB seq length: 0
Immum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	66.7	795	1 S73830	endopeptidase Ia (
2	41	65.1	351	1 SAVZV	surface antigen pr
3	41	65.1	351	1 SAVZMR	surface antigen pr
4	41	65.1	353	1 SAVZVC	surface antigen pr
5	41	65.1	354	2 S46877	B20R protein - var
6	41	65.1	354	2 T28616	hypothetical prote
7	41	65.1	355	2 D72174	D9R protein - vari
8	41	65.1	353	2 I39428	alcam - human
9	39	61.9	367	2 B31847	hypothetical prote
10	39	61.9	368	2 J70348	VSG expression sit
11	39	61.9	1014	2 S75724	hypothetical prote
12	38	60.3	129	2 I54411	MHC RT1-B A-alpha
13	38	60.3	221	1 HLMSA1	H-2 class II histo
14	38	60.3	233	2 I79358	IA-alpha class II histo
15	38	60.3	233	2 I79357	IA-alpha polypeptide
16	38	60.3	254	2 S11649	class II histocomp
17	38	60.3	256	1 HLMSA2	H-2 class II histo
18	38	60.3	256	2 S02855	class II histocomp
19	38	60.3	256	2 I54447	gene MHC H2-T-A-a1
20	38	60.3	258	1 HLMSAA	H-2 class II histo
21	38	60.3	310	2 A86812	sugar ABC transpor
22	38	60.3	454	2 A46532	ig mu chain C regi
23	38	60.3	490	2 A55141	GLCNAc beta-1,4-N-
24	38	60.3	526	2 A37821	butyrophilin - boy
25	38	60.3	530	2 S00163	glucuronosyltransf
26	38	60.3	555	2 JQ1526	interleukin-1 rece
27	38	60.3	754	2 S62512	probable cysteinyl
28	38	60.3	26926	1 I38344	titin, cardiac mus
29	37	58.7	235	2 F64799	hypothetical prote

30	37	58.7	235	2 C85565	probable tRNA ligase
31	37	58.7	691	2 D84889	receptor-
32	37	58.7	887	2 A46764	microsomal triglyc
33	37	58.7	894	2 I38047	triacylglyceride trans
34	37	58.7	895	2 A55413	triglyceride trans
35	37	58.7	1291	2 T09273	probable tail-host
36	37	58.7	1597	2 S65053	genome polyprotein
37	36	57.1	81	2 D81873	hypothetical prote
38	36	57.1	115	2 B46518	ig L1 chain V regi
39	36	57.1	182	2 A25468	T-cell surface gly
40	36	57.1	240	2 S01299	OX-45 membrane gly
41	36	57.1	391	2 H85063	hypothetical prote
42	36	57.1	447	2 T34992	probable lipoprote
43	36	57.1	515	2 S54592	hypothetical prote
44	36	57.1	520	2 H84663	probable cytochrom
45	36	57.1	577	2 I50731	ig heavy chain - n
46	36	57.1	628	2 C82039	conserved hypochet
47	36	57.1	729	2 A49120	fibroblast growth
48	36	57.1	776	2 S13470	isoamylase (EC 3.2
49	36	57.1	776	2 A37035	isoamylase (EC 3.2
50	36	57.1	837	2 T19825	hypothetical prote

ALIGNMENTS

RESULT 1
S73830
endopeptidase Ia (EC 3.4.21.53) - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: ATP-dependent proteinase I; ATP-dependent serine proteinase Ia;
M:Contains: adenosinetriphosphatase (EC 3.6.1.3)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 19-Jan-2001
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirki, E.; Li, B.C.; Herrmann, R.
C:Accession: S73830
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon
A:Reference number: S73327; MUID:97105885
A:Accession: S73830
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-795 <HIM>
A:Cross-references: EMBL:AE000050; GB:U00089; NID:G1674197; PIDN:AMB96152.1; PID:G167
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Comment: This enzyme catalyzes the hydrolysis of large proteins in the presence of
C:Genetics:
A:Gene: lon; F10_orf795
A:Superfamily: ATP-dependent serine proteinase Ia
C:Keywords: ATP; DNA binding; heat shock; hydrolase; nucleotide binding; P-loop; seri
F:379-386/Region: nucleotide-binding motif A (P-loop)
F:442-447/Region: nucleotide-binding motif B
F:702/Active site: Ser #status predicted

Query Match 66.7%; Score 42; DB 1; Length 795;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNMUTWRESK 11
DB 322 MNIPMWQESK 331

RESULT 2
SAVZV
surface antigen precursor - vaccinia virus
C:Species: vaccinia virus
A>Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jun-2000
C:Accession: A35522
R:Ueda, Y.; Morikawa, S.; Matsuura, Y.

Virology 177, 588-594, 1990
A:Title: Identification and nucleotide sequence of the gene encoding a surface antigen
A:Reference number: A35522; MID:90320131
A:Accession: A35522
A:Molecule type: mRNA
A:Residues: 1-351 <UEB>
A:Cross-references: EMBL:D90076; NID:q222769; PIDN:BAA14116.1; PID:q222770
C:Superfamily: vaccinia virus surface antigen; immunoglobulin homology
C:Keywords: glycoprotein; surface antigen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-351/Product: surface antigen #status predicted <SAT>
F:265-335/Domain: immunoglobulin homology <IMM>
F:117,182,261,269/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 65.1%; Score 41; DB 1; Length 351;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 NLTWYRESK 11
|:||||:|
DB 182 NITWYDKN 190

RESULT 3
SAV2WR
surface antigen precursor - vaccinia virus (strain WR)
N:Alternate names: B18R protein
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence, revision 30-Jun-1993 #text_change 16-Jun-2000
C:Accession: B38472; J01812; J00930
R:Smith, G.L.; Chan, Y.S.
J. Gen. Virol. 72, 511-518, 1991
A:Title: Two vaccinia virus proteins structurally related to the interleukin-1 receptor
A:Reference number: A38472; MID:91170931
A:Accession: B38472
A:Molecule type: DNA
A:Residues: 1-351 <SM1>
A:Cross-references: GB:D01019; NID:q222698; PIDN:BAA00826.1; PID:q222699
R:Smith, G.L.; Chan, Y.S.; Howard, S.T.
J. Gen. Virol. 72, 1349-1376, 1991
A:Title: Nucleotide sequence of 42kbp of vaccinia virus strain WR from near the right in
A:Reference number: J01767; MID:91259063
A:Accession: J01812
A:Molecule type: DNA
A:Residues: 1-351 <SM2>
A:Cross-references: DDBJ:D11079; NID:q222717; PIDN:BAA01848.1; PID:q222763; DDBJ:D01019;
C:Superfamily: vaccinia virus surface antigen; immunoglobulin homology
C:Keywords: glycoprotein; surface antigen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-351/Product: surface antigen #status predicted <SAT>
F:165-131/Domain: immunoglobulin homology <IMM1>
F:165-223/Domain: immunoglobulin homology <IMM2>
F:265-335/Domain: immunoglobulin homology <IMM3>
F:73-129,172-221,272-333/Disulfide bonds: #status predicted
F:117,182,261,269/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 65.1%; Score 41; DB 1; Length 351;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 NLTWYRESK 11
|:||||:|
DB 182 NITWYDKN 190

RESULT 4
SAV2VC
surface antigen precursor - vaccinia virus (strain Copenhagen)
C:Species: vaccinia virus
A:Note: host Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence, revision 30-Sep-1991 #text_change 21-Jan-2000
C:Accession: I42527
R:Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paolletti, E.
Virology 179, 517-563, 1990
A:Title: Appendix to "The complete DNA sequence of vaccinia virus".
A:Reference number: A42501
A:Accession: I42527
A:Molecule type: DNA
A:Residues: 1-353 <GCE>
A:Cross-references: GB:M35027; NID:q335317; PIDN:AAA48218.1; PID:q335566
R:Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paolletti, E.
Virology 179, 247-266, 1990
A:Title: The complete DNA sequence of vaccinia virus.
A:Reference number: A42531; MID:91021027
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
C:Superfamily: vaccinia virus surface antigen; immunoglobulin homology
C:Keywords: glycoprotein; surface antigen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-353/Product: surface antigen #status predicted <SAT>
F:267-337/Domain: immunoglobulin homology <IMM>
F:119,184,263,271/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 65.1%; Score 41; DB 1; Length 353;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 NLTWYRESK 11
|:||||:|
DB 184 NITWYDKN 192

RESULT 5
B2OR
protein - variola virus
N:Alternate names: B19R protein (COP)
C:Species: variola virus
C:Date: 06-Jan-1995 #sequence, revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S46877; B36857
R:Kolymhalov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F
submitted to the EMBL Data Library, April 1992
A:Description: Nucleotide sequence analysis of the region of variola virus xhoI F O H
A:Reference number: S46868
A:Accession: S46877
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <KOL>
A:Cross-references: EMBL:X67117; NID:q516428; PIDN:CAA47529.1; PID:q516438
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Reference number: A36859
A:Accession: B36857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <BLI>
A:Cross-references: GB:X69198; NID:q456758; PIDN:CAA49129.1; PID:q457079
A:Experimental source: strain India-1967 sep. major isolate ind3
C:Superfamily: vaccinia virus surface antigen; immunoglobulin homology
F:268-338/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 41; DB 2; Length 354;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 NLTWYRESK 11
|:||||:|
DB 185 NITWYDKN 193

RESULT 6

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2002, 10:37:27 ; Search time 85.5 Seconds
(without alignments)
4.717 Million cell updates/sec

Title: US-09-281-760c-5
Sequence: 1 GMMITWRESK 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Immun DB seq length: 0
Immun DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	66.7	795	1 LON_MYCPN	P78025 mycoplasma
2	41	65.1	351	1 VB19_VACCD	P23998 vaccinia vi
3	41	65.1	351	1 VB19_VACCV	P25213 vaccinia vi
4	41	65.1	351	1 VB19_VAVR	P33795 variola vir
5	41	65.1	353	1 VB19_VACCC	P21077 vaccinia vi
6	41	65.1	583	1 C166_HUMAN	Q13740 homo sapien
7	41	65.1	583	1 C166_MOUSE	Q61490 mus musculu
8	38	60.3	221	1 HA2Q_MOUSE	P04227 mus musculu
9	38	60.3	227	1 HA2F_MOUSE	P14438 mus musculu
10	38	60.3	233	1 HA2F_MOUSE	P14435 mus musculu
11	38	60.3	233	1 HA2S_MOUSE	P14436 mus musculu
12	38	60.3	233	1 HA2R_MOUSE	P14437 mus musculu
13	38	60.3	254	1 HA2I_MOUSE	P23150 mus musculu
14	38	60.3	256	1 HA2B_MOUSE	P14434 mus musculu
15	38	60.3	256	1 HA2B_RAT	P20037 rattus norv
16	38	60.3	256	1 HA2D_MOUSE	P04228 mus musculu
17	38	60.3	256	1 HA2K_MOUSE	P01910 mus musculu
18	38	60.3	490	1 BAGT_LYMT	Q09323 lymanea sta
19	38	60.3	526	1 BPTT_BOVIN	P18892 bos taurus
20	38	60.3	530	1 UBPS_MOUSE	P17717 mus musculu
21	38	60.3	754	1 YAF6_MOUSE	Q09860 scizosacch
22	37	58.7	235	1 YAF6_SCHRO	P77427 escherichia
23	37	58.7	235	1 YAF6_ECOLI	P55156 bos taurus
24	37	58.7	887	1 MTP_BOVIN	P55157 homo sapien
25	37	58.7	894	1 MTP_HUMAN	O08601 mus musculu
26	37	58.7	895	1 MTP_MESAU	P55158 mesocricetu
27	37	58.7	1597	1 RRPQ_CRMV	Q66220 chinese rap
28	36	57.1	182	1 CD3G_HUMAN	P09693 homo sapien
29	36	57.1	240	1 CD48_RAT	P10252 rattus norv
30	36	57.1	515	1 YH60_EAST	Q03264 saccharomyc
31	36	57.1	730	1 FGRL_DROME	Q07407 drosophila
32	36	57.1	776	1 ISOA_PSEAY	P10342 pseudomonas
33	36	57.1	776	1 ISOA_PSESP	P26501 pseudomonas

34	36	57.1	837	1 YLE5_CAEEL	P46941 caenorhabdi
35	35	55.6	180	1 RL5_CHLMU	Q9pjm6 chlamydia m
36	35	55.6	180	1 RL5_CHLFR	P28531 chlamydia t
37	35	55.6	370	1 HVCI_HEPFR	P23084 heterodonu
38	35	55.6	393	1 HVCS_HEPFR	P23086 heterodonu
39	35	55.6	406	1 YNQS_YEAST	P53891 saccharomyc
40	35	55.6	421	1 O67B_DROME	Q9vlt20 drosophila
41	35	55.6	438	1 HVCS_HETER	P23085 heterodonu
42	35	55.6	481	1 HVCS_HETER	P23087 heterodonu
43	35	55.6	461	1 XYLB_LACIA	P23088 heterodonu
44	35	55.6	501	1 XYLB_LACIA	Q9cfcg8 lactococcus
45	35	55.6	531	1 YP60_MERTM	P14933 methanobact
46	35	55.6	543	1 APPA_BACSU	P42061 bacillus su
47	35	55.6	706	1 NUCL_HUMAN	P19338 homo sapien
48	35	55.6	712	1 NUCL_RAT	P13383 rattus norv
49	35	55.6	712	1 NUCL_MESAU	P08199 mesocricetu
50	35	55.6	795	1 LON_MYCCE	P47481 mycoplasma

ALIGNMENTS

RESULT 1
LON_MYCPN STANDARD; PRT: 795 AA.
ID LON_MYCPN
AC P78025;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53).
GN LON OR MPN332 OR MP504.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; Pubmed=6948633;
RA Himmelfreid R., Hilbert H., Plagens H., Plirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS
CC IN PRESENCE OF ATP. DEGRADATES THE REGULATORY PROTEINS RCSA AND
CC SULA. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
CC PROTEIN SUBSTRATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
CC CASEIN AND DENATURATED SERUM ALBUMIN, IN PRESENCE OF ATP.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOSOL.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE000050; AAB96152.1; -.
CC MEROPS; S16.004; -.
DR InterPro: IPR003593; AAA.
DR InterPro: IPR001939; AAA subfam.
DR InterPro: IPR001687; ATP_GTP_A.
DR InterPro: IPR003111; LON.
DR InterPro: IPR001984; Lon_endopep.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF02190; LON; 1.
DR PRINTS; PR00830; ENDOLAPTASE.

DR	SMART; SM00382; AAA; 1.	
DR	SMART; SM00464; LON; 1.	
KM	PROSTITE; PS01046; LON_SER; 1.	
KM	HYDROLASE; Serine protease; ATP-binding; Complete proteome	
FT	DOMAIN	POLY-SER.
FT	304	388
FT	379	386
FT	ACT_SITE	ATP (POTENTIAL).
FT	952	702
SC	SEQUENCE	755 AA; 92023 MW; 7E76B50820600C891 CRC64;

	66.7%;	Score 42;	DB 1;	Length 795;
Best Local Similarity	Pred. No. 6.7;			
Matches	Conservative 7;	Mismatches 1;	Indels 0;	Gaps 0.
OY .	2 NNTVYSKSK 11			
	:::			
Dd	322 NNTRPMDESK 331			

RESULT	2
ID	VBI9_VACCD
AC	P2398;
DT	01-MAR-1992 (Rel. 21, Created)
DT	01-MAR-1992 (Rel. 21, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	SURFACE ANTIGEN S PRECURSOR (S ANTIGEN).
OS	B19R.
GN	Vaccinia virus (strain Dairén I).
OC	Viruses; dsRNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Orthopoxvirus.
OX	NCB1_TaxID=10260;
RN	[1]
RP	SEQUENCE FROM N.A.
FX	MEDLINE=90320131. PubMed=2196742;
RA	Ueda Y., Morikawa S., Matsura Y.,
RT	"Identification and nucleotide sequence of the gene encoding a surface antigen induced by vaccinia virus.";
RL	Virology 177:588-594(1990).
CC	-I- EDITION: MAY BIND INTERLEUKIN-1 AND/OR INTERLEUKIN-6 AND PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS. IN CONSEQUENCE THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED AND VIRUS REPLICATION ENHANCED.
CC	-I- SUBCELLULAR LOCATION: INDUCED ON THE SURFACE OF VACCINIA VIRUS-INFECTED CELLS.
CC	-I- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC	-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC	-I- SIMILARITY: TO THE INTERLEUKIN-1 RECEPTOR.
CC	----- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (http://www.isb-sib.ch/announce/ or_send_an_email_to_license@sib.ch). -----
CC	EMBL, D90076; BAA14116.1; .
DR	PIR, A35522; SAVZVV.
DR	InterPro: IPRO03006; IG_MHC.
DR	InterPro: IPRO03600; IG_like. Pfam: PF00047; Ig; 2.
DR	SMART: SM00410; IG_Like; 1.
KM	Immunoglobulin domain; Antigen; Glycoprotein; Signal; Early protein. POTENTIAL.
FT	SIGNAL 1 19
FT	CHAIN 20 351
FT	DOMAIN 65 137
FT	DOMAIN 164 229
FT	DOMAIN 264 341
FT	DISULEID 73 129
FT	DISULEID 172 221
FT	DISULEID 272 333
FT	SHORT 117 117
FT	----- SOURCE ANTIGEN S IG-LIKE C2-TYPE DOMAIN 1. IG-LIKE C2-TYPE DOMAIN 2. IG-LIKE V-TYPE DOMAIN. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC...) (POTENTIAL). -----

SEQ	351 AA:	40701 MW:	20997567D39E7DB CR664:
FT CARBOHYD	182	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	182	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	261	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	269	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT CARBOHYD	321	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SEQUENCE	351 AA:	40701 MW:	20997567D39E7DB CR664:

	65.1%;	Score 41;	DB 1;	Length 351;
Query Match	Best Local Similarity	55.6%;	Pred. No. 4.4;	
Matches	5;	Conservative	0;	Mismatches
			Indels	0;
Gaps	0;			
OY	3	NLWYRREK	11	
	:: :: :: ::			
Db	182	NITWYKDOK	190	

RESULT	3
VB19_VACCV	STANDARD: PRT; 351 AA.
ID	VB19_VACCV
AC	P25213;
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)
DE	SURFACE ANTIGEN S PRECURSOR (S ANTIGEN).
GN	B19R OR B18R.
OS	Vaccinia virus (strain WR).
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC	Orthopoxvirus.
OX	NCBI_Taxid=10254;
ON	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91259063; Pubmed=2045793;
RA	Smith G.L., Chan Y.S., Howard S.T.;
RT	"Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near
RL	the right inverted terminal repeat.";
RL	J. Gen. Virol. 72:1349-1376(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91170911; Pubmed=1826022;
RA	Smith G.L., Chan Y.S.;
RT	"Two vaccinia virus proteins structurally related to the
RL	interleukin-1 receptor and the immunoglobulin superfamily.";
RL	J. Gen. Virol. 72:511-518(1991).
CC	- I- FUNCTION: MAY BIND INTERLEUKIN-1 AND/OR INTERLEUKIN-6 AND PREVENT
CC	THE CYTOKINES REACHING THEIR NATURAL RECEPTORS. IN CONSEQUENCE
CC	THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED AND VIRUS
CC	REPLICATION ENHANCED.
CC	- I- SUBCELLULAR LOCATION: INDUCED ON THE SURFACE OF VACCINIA
CC	VIRUS INFECTED CELLS.
CC	- I- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC	- I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC	- I- SIMILARITY: TO THE INTERLEUKIN-1 RECEPTOR.
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (See http://www.isb-sib.ch/commence/
CC	or send an email to license@sib-sib.ch).
CC	EMBL: D11079; BAA01848.1; -
CC	EMBL: D01019; BAA00826.1; -
CC	EMBL: X56122; CAA39587.1; -
CC	EMBL: A19579; CAA01478.1; -
CC	PIR: B38472; JAVZMR.
CC	PIR: J01812; J01812.
CC	InterPro: IPR003006; Ig_MHC.
CC	InterPro: IPR003600; Ig_Like.
CC	Pfam: PF00047; Ig; 2.
CC	SMART: SM00410; Ig_Like; 1.
CC	Immunoglobulin domain; Antigen; Glycoprotein; Signal; Early protein.
CC	SIGNAL 1 19 POTENTIAL.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:35:54 ; Search time 191.29 Seconds
(without alignments)
8.411 Million cell updates/sec

Title: US-09-281-760C-5
Perfect score: 63
Sequence: 1 GMMLTWRESK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

imum DB seq length: 0
imum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOCTIST:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	42	66.7	380	2	09S405
2	41	65.1	113	6	09BDE7
3	41	65.1	265	12	09DUN2
4	41	65.1	315	12	09IFU7
5	41	65.1	351	12	072754
6	41	65.1	353	12	09JF34
7	41	65.1	354	12	089115
8	41	65.1	355	12	089923
9	41	65.1	521	6	046634
10	41	65.1	521	6	046651
11	41	65.1	583	6	09BH13
12	41	65.1	583	11	035112
13	40	63.5	541	5	09NA52
14	39	61.9	191	5	076423
15	39	61.9	244	5	076422
16	39	61.9	275	11	09JK39
17	39	61.9	311	2	09FA46
18	39	61.9	367	5	026723
19	39	61.9	368	5	026748

20	39	61.9	1014	2	055374	055374 synechocyst
21	39	61.9	2196	3	09HDV6	09hdv6 schizosacch
22	38	60.3	63	7	09TPJ8	09tpj8 anguilla sp
23	38	60.3	63	7	09TPG1	09tpg1 salarias sp
24	38	60.3	129	7	031259	031259 rattus norv
25	38	60.3	129	7	031264	031264 rattus norv
26	38	60.3	227	7	031247	031247 peromyscus
27	38	60.3	240	11	09DCS4	09dcs4 mus musculu
28	38	60.3	254	7	09TG72	09tg72 mus musculu
29	38	60.3	254	7	09TG71	09tg71 mus musculu
30	38	60.3	286	6	046535	046535 bos taurus
31	38	60.3	310	2	09CFH9	09cfh9 lactococcus
32	38	60.3	529	11	09PC18	09pc18 mus musculu
33	38	60.3	555	13	090874	090874 gallus gall
34	38	60.3	4650	4	013598	013598 homo sapien
35	38	60.3	26926	4	010466	010466 homo sapien
36	37	58.7	252	2	P94681	P94681 comamonas t
37	37	58.7	312	12	089122	089122 crucifer to
38	37	58.7	467	2	069452	069452 mycoplasma
39	37	58.7	651	10	022138	022138 arabidopsis
40	37	58.7	854	12	09WC85	09wc85 human immun
41	37	58.7	1291	9	064295	064295 streptococc
42	36	57.1	81	2	09JUY8	09juy8 neisseria m
43	36	57.1	151	5	09NBB7	09nbb7 drosophila
44	36	57.1	181	4	09BS46	09bs46 homo sapien
45	36	57.1	324	1	09HTW9	09htw9 thermoplasm
46	36	57.1	391	10	09S9T0	09s9t0 arabidopsis
47	36	57.1	447	2	086673	086673 streptomyce
48	36	57.1	491	12	039819	039819 equine rota
49	36	57.1	491	12	039820	039820 equine rota
50	36	57.1	491	12	039821	039821 equine rota

ALIGNMENTS

RESULT 1
ID 09S405 PRELIMINARY; PRT; 380 AA.
AC 09S405;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TERA.
GN TERA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBL_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S2;
RA Topchieva A., Bryden L.J., Taylor D.E., Hoffman P.S.;
RT "Characterization of the chromosomal tellurite resistance gene cluster
in Proteus mirabilis.";
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AP168355; AAD47285.1; -
DR InterPro: IPR003325; TcrD.
DR Pfam: PF02342; TcrD; 2.
SQ SEQUENCE 380 AA; 41562 MW; 941B4BC7D33B2DE CRC64;

Query Match 66.7%; Score 42; DB 2; Length 380;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MMLTWRESK 11
DB 204 INLDWRESK 213

RESULT 2
Q9BDE7

ID Q9BDE7 PRELIMINARY; PRT; 113 AA.
 AC Q9BDE7;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE ACTIVATED LEUKOCYTE CELL ADHESION MOLECULE (FRAGMENT).
 GN ALCAM.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=bone marrow;
 RA Ringe J., Kaps C., Schmitt B., Buescher K., Bartel J., Smolian H.,
 RA Schultz O., Burmester G.R., Haupl T., Sittlinger M.;
 RT "Porcine Mesenchymal Stem Cells: Induction of distinct mesenchymal
 cell lineages";
 RT Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 EMBL: AJ311681; CCNC35029.1; --
 FT NON_TER 113
 FT NON_TER 1
 SQ SEQUENCE 113 AA; 12786 MW; E4701124906F443F CRC64;

Query Match 65.1%; Score 41; DB 6; Length 113;
 Best Local Similarity 66.7%; Pred. No. 4.9;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 NLWYRESK 11
 :|||||
 Db 105 NITWYRNGK 113

RESULT 3
 Q9DUN2 PRELIMINARY; PRT; 265 AA.
 ID Q9DUN2;
 AC Q9DUN2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERFERON-ALPHA/BETA RECEPTOR.
 GN B18R.
 OS Vaccinia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WEITH;
 RX PubMed=11070021;
 RA Alcaml A., Symons J.A., Smith G.L.;
 RA "The vaccinia virus soluble alpha/beta interferon (IFN) receptor binds
 RT to the cell surface and protects cells from the antiviral effects of
 RT IFN";
 RT J. Virol. 74:11230-11239(2000).
 RL -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AJ269556; CAC16604.1; --
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1
 DR SMART: SMO0410; Ig_Like; 1.
 KW Receptor.
 SQ SEQUENCE 265 AA; 31038 MW; BA4AE8DA1A1A9 CRC64;

Query Match 65.1%; Score 41; DB 12; Length 265;
 Best Local Similarity 55.6%; Pred. No. 12;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 NLWYRESK 11
 :|||||

Db 184 NITWYKDNK 192
 RESULT 4
 Q9IFU7 PRELIMINARY; PRT; 315 AA.
 ID Q9IFU7;
 AC Q9IFU7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SOLUBLE IFN RECEPTOR (FRAGMENT).
 OS Bean 58058 virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=67082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marques J.T., Daponseca F.G., Kroon E.G.;
 RT "The genome of Bean 58058 virus contains a gene homologous to Vaccinia
 virus B18R gene";
 RT Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 RL -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF261890; AAF74754.1; --
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SMO0410; Ig_Like; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 315 AA; 36544 MW; AAAC6CBDA69095AA CRC64;

Query Match 65.1%; Score 41; DB 12; Length 315;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 NLWYRESK 11
 :|||||
 Db 157 NITWYKDNK 165

RESULT 5
 Q72754 PRELIMINARY; PRT; 351 AA.
 ID Q72754;
 AC Q72754;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE B17R PROTEIN.
 GN B17R.
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GRI-90;
 RX MEDLINE=98229462; PubMed=9568042;
 RA Shchelkunov S.N., Safonov P.F., Totmenin A.V., Petrov N.A.,
 RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
 RA "The genomic sequence analysis of the left and right species-specific
 RT terminal region of a cowpox virus strain reveals unique sequences and
 RT a cluster of intact ORFs for immunomodulatory and host range
 RT proteins";
 RT Virology 243:432-460(1998).
 RL -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: Y15035; CAA75293.1; --
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.

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OM protein - protein search, using sw_model

Run on: April 21, 2002, 10:38:47 ; Search time 23.48 Seconds
(without alignments)
4.792 Million cell updates/sec

Title: US-09-281-760C-2
Perfect score: 18
Sequence: 1 YRXXL 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 16280

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents.AA.*
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2.6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2.6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	77.8	5	2	US-08-968-676-25 Sequence 25, Appl
2	12	66.7	2	4	US-09-214-614-2 Sequence 2, Appl
3	12	66.7	3	1	US-08-968-676-27 Sequence 27, Appl
4	12	66.7	4	1	US-08-240-712-4 Sequence 4, Appl
5	12	66.7	4	1	US-08-428-488-59 Sequence 59, Appl
6	12	66.7	4	1	US-08-428-488-60 Sequence 60, Appl
7	12	66.7	4	1	US-08-428-488-61 Sequence 61, Appl
8	12	66.7	4	1	US-08-428-488-62 Sequence 62, Appl
9	12	66.7	4	1	US-08-428-488-63 Sequence 63, Appl
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11	12	66.7	4	1	US-08-428-488-65 Sequence 65, Appl
12	12	66.7	4	1	US-08-428-488-66 Sequence 66, Appl
13	12	66.7	4	1	US-08-428-488-67 Sequence 67, Appl
14	12	66.7	4	1	US-08-428-488-68 Sequence 68, Appl
15	12	66.7	4	1	US-08-428-488-69 Sequence 69, Appl
16	12	66.7	4	1	US-08-428-488-70 Sequence 70, Appl
17	12	66.7	4	1	US-08-428-488-71 Sequence 71, Appl
18	12	66.7	4	1	US-08-428-488-72 Sequence 72, Appl
19	12	66.7	4	1	US-08-428-488-73 Sequence 73, Appl
20	12	66.7	4	1	US-08-428-488-74 Sequence 74, Appl
21	12	66.7	4	1	US-08-253-272-22 Sequence 22, Appl
22	12	66.7	4	1	US-08-335-198-25 Sequence 25, Appl
23	12	66.7	4	1	US-08-429-732-20 Sequence 20, Appl
24	12	66.7	4	1	US-08-203-806B-15 Sequence 15, Appl
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33	12	66.7	4	2	US-08-473-022-2 Sequence 2, Appl
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38	12	66.7	4	2	US-08-685-589A-62 Sequence 62, Appl
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49	12	66.7	4	5	PCT-US93-01669-16 Sequence 16, Appl
50	12	66.7	4	5	PCT-US96-08798-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-968-676-25
Sequence 25, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-25

Query Match 77.8%; Score 14; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.0e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YRXL 5
1 YRML 5

US-09-214-614-2
Sequence 2, Application US/09214614
Patent No. 6225100

GENERAL INFORMATION:
APPLICANT: Grund, Alan D.
TITLE OF INVENTION: NOVEL ARTISULFOTRANSFERASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/214,614
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 3161-15-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-214-614-2

Query Match 66.7%; Score 12; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YR 2
1 YR 2

US-08-968-676-27
Sequence 27, Application US/08968676
Patent No. 5919639

GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA

ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-27

Query Match 66.7%; Score 12; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YR 2
1 YR 2

US-08-240-712-4
Sequence 4, Application US/08240712
Patent No. 5599907

GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2002, 10:38:11 ; Search time 40.45 Seconds
(without alignments)
9.156 Million cell updates/sec

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Perfect score: 18
Sequence: 1 YRXXL 5
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Gapop 10.0 , Gapext 0.5

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imum DB seq length: 5
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 50 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
1	14	77.8	5	2	ADP10205	Leu-enkephalin.	
2	14	77.8	5	11	AAR08321	Peptide with opio	
3	14	77.8	5	15	AARS5499	Opioid oligopeptid	
4	14	77.8	5	15	AARS5508	Opioid oligopeptid	
5	14	77.8	5	15	AARS5490	Opioid oligopeptid	
6	14	77.8	5	19	AAW47949	AEI1 analogue eff	
7	14	77.8	5	21	AAV69582	Generic immunogen	
8	13	72.2	5	22	AAAB81468	Synthetic peptide	
9	12	66.7	2	22	AAAB9138	Opioid peptide seq	
10	12	66.7	3	18	AAW33241	Analgasic peptide	
11	12	66.7	3	19	AAW56224	Anti-Inflammatory	

50	12	66.7	4	15	AAR55477	Opioid oligopeptid
49	12	66.7	4	15	AAR55475	Opioid oligopeptid
48	12	66.7	4	15	AAR55473	Opioid oligopeptid
47	12	66.7	4	15	AAR55471	Opioid oligopeptid
46	12	66.7	4	15	AAR55469	Opioid oligopeptid
45	12	66.7	4	15	AAR55467	Opioid oligopeptid
44	12	66.7	4	15	AAR55465	Opioid oligopeptid
43	12	66.7	4	15	AAR55494	Opioid oligopeptid
42	12	66.7	4	15	AAR55493	Opioid oligopeptid
41	12	66.7	4	15	AAR55489	Opioid oligopeptid
40	12	66.7	4	15	AAR55488	Opioid oligopeptid
39	12	66.7	4	15	AAR55485	Opioid oligopeptid
38	12	66.7	4	15	AAR55484	Opioid oligopeptid
37	12	66.7	4	15	AAR55481	Opioid oligopeptid
36	12	66.7	4	15	AAR55507	Opioid oligopeptid
35	12	66.7	4	15	AAR55506	Opioid oligopeptid
34	12	66.7	4	15	AAR55503	Opioid oligopeptid
33	12	66.7	4	15	AAR55502	Opioid oligopeptid
32	12	66.7	4	15	AAR55498	Opioid oligopeptid
31	12	66.7	4	15	AAR55497	Opioid oligopeptid
30	12	66.7	4	15	AAR51595	Peptide analogue #
29	12	66.7	4	15	AAW51589	Peptide analogue #
28	12	66.7	4	15	AAW51593	Peptide analogue #
27	12	66.7	4	14	AAR38136	Protease-non-labile
26	12	66.7	4	14	AAR33664	Growth hormone rel
25	12	66.7	4	14	AAR33660	Growth hormone rel
24	12	66.7	4	14	AAR41643	Internalisation si
23	12	66.7	4	13	AAR24410	Cpase B-like enzym
22	12	66.7	4	13	AAR3084	Fluorinated peptid
21	12	66.7	4	8	AAW71700	Analgesic peptide
20	12	66.7	4	8	AAW71582	Growth hormone rel
19	12	66.7	4	8	AAW71580	Growth hormone rel
18	12	66.7	4	8	AAW61741	Analgesic peptide
17	12	66.7	4	7	AAW61741	Analgesic peptide
16	12	66.7	4	7	AAW61491	Analgesic tetrapep
15	12	66.7	4	6	AAW50690	Analgesic enkephal
14	12	66.7	4	6	AAW50336	Analgesic enkephal
13	12	66.7	4	5	AAW40467	Opioid peptide seq
12	12	66.7	3	22	AAAB91597	Opioid peptide seq

ALIGNMENTS

RESULT

ID	AA10205 standard; Protein; 5 AA.
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AC AAP10205;

DT 16-DEC-1992 (first entry)

Leu-enkephalin.

KW Analgesic; enkephalin.

Synthetic.

Key	Location/Qualifiers
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/note= "D- or L-form residue"

PN JP56045450-A.

PD 25-APR-198

PF 21-SEP-1979; 79JP-0121654

PR 21-SEP-1979; 79JP-0121654

PA (DAUC) DAIICHI SELYAKU KK.
XX

DR WPL; 1981-43030D/24 (43030D)

XX Analgesic penta-peptide - comprising tyrosine, arginine, glycine,
PT phenylalanine with methionine or leucine hydroxyl or amine
XX
XX
PS Disclosure; Page 3; 7pp; Japanese.
XX
XX The peptide is a leucine-enkephalin analogue, opt. having the
CC C-terminal amidated. It is an analgesic having stronger activity
CC compared with the enkephalins.
CC It is pred. by conventional chemical synthesis, either in liq.
CC phase or solid phase.
XX
XX
SQ Sequence 5 AA:

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Query Match      77.8%   Score 14; DB 2; Length 5;
Best local Similarity 60.0%   Pred. No. 4.3e+05;
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      1 1 1
Db 1 yrgfl 5

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AA080321;	
05-FEB-1991	(first entry)
Peptide with opioid activity.	
Analgesic.	
Synthetic.	
Key	Location/Qualifiers
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/label= D-Arg	
Misc-difference	4
/label= Phe or Phe(NO2) or Neph	
Misc-difference	5
/label= -NH-CH-CH2-CH(CH3)2-X or -Leu-NH-CH2-X	
or -NH-CH2-X	
/note= "X" = -N-(2-(3-nitro-2-pyridyl)ethoxy)amide"	
JF02233694-A.	
17-SEP-1990.	
07-MAR-1989;	89JP-0052901.
07-MAR-1989;	89JP-0052901.
(VITA-) VITAMINE KENKYUSHO.	
WPI; 1990-325185/43.	
New peptide and its pharmaceutically acceptable salts - has opioid action, useful for analgesics	
Claim 1; Page 861; 5pp; Japanese.	
Peptide has opioid activity, useful in analgesics.	

	Matches	3;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	YRXXL	5							
Db	1	YRGL	5							

RESULT	3
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ID	AA85499 standard; peptide; 5 AA.
XX	
AC	AA85499;
XX	
DT	19-DEC-1994 (first entry)
DE	Opitoid oligopeptide.
XX	
KW	opitoid receptor; analgesic; antitussive; antidiarrhoeal; antitumour; pain killer.
XX	

FN	Key	Location/Qualifiers
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XX	WO9411018-A.	
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PD	26-MAY-1994.	
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PF	04-NOV-1993;	93MO-US10711.
XX		
PR	12-NOV-1992;	92US-0974943.
XX		
XX		(BIOM-) BIOMEASURE INC.
XX		
PA	Kim SH, Moreau J, Taylor JE;	
PI		
DR	WPI; 1994-183155/22.	
XX		
FT	New opioid oligo-peptide cpds. - having analgesic, antitussive, antidiarrhoeal and antitumour activity	
XX		
PS	Claim 16; Page 39; 45pp; English.	
XX		
CC	This peptide is an example of a highly generic formula representing opioid oligopeptides which selectively bind to receptors on cells.	
CC	The peptides have analgesic, antitussive and antidiarrhoeal activity.	
CC	They can also be used for treating various cancers such as lung or breast cancer, melanoma or neuroblastoma, and as tools for detecting specific opioid receptors.	
XX		
XO	Sequence 5 AA;	

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Best Local Similarity	80.08;	Pred. No. 4.3e+05;		
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			Gaps	0;

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Db	1 yrxf1 5

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Copyright (c) 1993 - 2000 Compugen Ltd.

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Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Minimum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SPTREMBL.17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult	Score	Query Match	Length	DB	ID	Description
1	4	22.2	4	11	Q08433	Q08433 rattus norv
2	3	16.7	5	13	P82070	P82070 litorea rub
3	3	16.7	5	13	P82071	P82071 litorea rub
4	3	16.7	5	13	P82072	P82072 litorea rub
5	3	16.7	5	13	P82073	P82073 litorea rub
6	3	16.7	5	13	P82099	P82099 litorea rub
7	3	16.7	5	13	P82100	P82100 litorea rub
8	2	11.1	5	10	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
Q08433 1
AC Q08433: PRELIMINARY: PRT: 4 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSO MAL (EC 2.4.1.17) (UDPCT)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RL hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROSO ME.
DR EMBL; S38636; AAB19259.1;
FW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 22.2%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 L 5
Db 3 L 3

RESULT 2
P82070 1
ID P82070: PRELIMINARY: PRT: 5 AA.
AC P82070;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELIDIN 1.1.
OS Litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litorea.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinboerner S.T., Mabnitz P.A., Maugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litorea rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTI-BIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 Y 1

Db 3 F 3

RESULT 3
P82071 PRELIMINARY; PRT: 5 AA.

AC P82071; 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1].
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
Litoria rubella", the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RT Aust. J. Chem. 49:955-963(1996).
RL -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=626; METHOD=FPAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA: 626 MW: 6DD9C9CB10300000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
Db 3 F 3

RESULT 4
P82072 PRELIMINARY; PRT: 5 AA.

AC P82072; 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
RUBELLIDIN 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1].
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
Litoria rubella", the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RT Aust. J. Chem. 49:955-963(1996).
RL -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FPAB.
KW Amphibian skin; Amidation.
SQ SEQUENCE 5 AA: 656 MW: 71A9C9CB10300000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
Db 3 F 3

RESULT 5
P82073 PRELIMINARY; PRT: 5 AA.

AC P82073; 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
RUBELLIDIN 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1].
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RT Aust. J. Chem. 52:0-0(1999).
RL -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC Amphibian skin.
KW Amphibian skin.
SQ SEQUENCE 5 AA: 570 MW: 71A9C9CB62A00000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
Db 3 F 3

RESULT 6
P82099 PRELIMINARY; PRT: 5 AA.

AC P82099; 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1].
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";
RT Aust. J. Chem. 52:0-0(1999).
RL Amphibian skin; Amidation.
KW Amphibian skin; Amidation.
SQ SEQUENCE 5 AA: 630 MW: 66B761F2C9A00000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:44:57 ; Search time 17.3 Seconds

(without alignments)
10.597 Million cell updates/sec

Title: US-09-281-760C-2

Perfect score: 18

Sequence: 1 YRXXL 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 29

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	44.4	5	1	AL14_CARMA
2	7	38.9	4	1	P81817 carcinus ma
3	7	38.9	4	1	P42562 hirudo medi
4	7	38.9	5	1	P42563 hirudo medi
5	7	38.9	5	1	P41853 artiposthi
6	7	38.9	5	1	P01373 periplaneta
7	7	38.9	5	1	P58261 daucus caro
8	5	27.8	4	1	FLRF_HIRME
9	5	27.8	4	1	FMRF_MACNI
10	5	27.8	4	1	TUFT_HUMAN
11	5	27.8	5	1	BIOB_SALTY
12	5	27.8	5	1	UF01_MOUSE
13	4	22.2	3	1	GRMA_HUMAN
14	3	16.7	4	1	ACH1_ACHFU
15	3	16.7	5	1	PAP2_PARMA
16	3	16.7	5	1	SUGA_ACHDO
17	3	16.7	5	1	TPIS_CANFA
18	3	16.7	5	1	UC32_MAIZE
19	2	11.1	3	1	LUXE_VIBFI
20	2	11.1	3	1	THYL_PIG
21	2	11.1	4	1	DCML_PSECH
22	2	11.1	4	1	DCMS_PSECH
23	2	11.1	5	1	BIOA_CITFR
24	2	11.1	5	1	BIOA_SALTY
25	2	11.1	5	1	BIOB_CITFR
26	2	11.1	5	1	BPP7_BOTIN
27	2	11.1	5	1	TRM3_ECOLI
28	1	5.6	4	1	EOSI_HUMAN
29	0	0.0	4	1	RM01_YEAST
			5	1	UXA4_CHLTR
					P38005 chlamydia t

ALIGNMENTS

RESULT 1
AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINOSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
[1]
RN
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvre H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorppe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTROPHIC FACTOR OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5
FT SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 44.4%; Score 8; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 YRXXL 5
DB 1 YSFG 5

RESULT 2
FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchochordata; Hirudiniiformes; Hirudiniidae; Hirudo.
OX NCBI_TaxID=6421;
RN
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
FT SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
DB 1 Y 1

```
RESULT 3
FAM4_HIRME STANDARD; PRT: 4 AA.
ID FAM4_HIRME
AC P43563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YMRF-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
DE Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OC Arynchobdellida; Hirudinoformes; Hirudindae; Hirudo.
OX NCBI_Taxid=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; Pubmed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -1- SIMILARITY: BELONGS TO THE FAM4 (FMRFAMIDE RELATED PEPTIDE)
FAMILY
CC Neuropeptide; Amidation.
KW MOD_RES 4 AA; 616 MW; 69D4068B3000000 CRC64;
SQ SEQUENCE 4 AA; 616 MW; 69D4068B3000000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 Y 1
DB 1 Y 1

RESULT 4
FAM4_ARTTR STANDARD; PRT: 5 AA.
ID FAM4_ARTTR
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE RYRIF-AMIDE.
OS Artiosopstha triangulata
DE Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
OC Rhabdiphora; Sericata; Tricladida; Tricicola; Geoplanidae;
OC Rhabdiphorus
OX NCBI_Taxid=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; Pubmed=7909164;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYRIFamide: a turbellarian FMRFamide-related peptide (FAM4).";
RL Regul. Pept. 50:37-43(1994).
CC -1- SIMILARITY: BELONGS TO THE FAM4 (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
CC Neuropeptide; Amidation.
KW MOD_RES 5 AA; 754 MW; 69D404BA4600000 CRC64;
SQ SEQUENCE 5 AA; 754 MW; 69D404BA4600000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 Y 1
DB 2 Y 2

RESULT 5
PRTCT_PERAM STANDARD; PRT: 5 AA.
ID PRTCT_PERAM
AC P41373;
```

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE PROCTOLIN.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OX Blattodea; Blattidae; Periplaneta.
OX NCBI_Taxid=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES-P. americana;
RX MEDLINE=76074708; Pubmed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES-P. americana;
RX MEDLINE=81225865; Pubmed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES-L. polyphemus;
RX MEDLINE=90287800; Pubmed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES-C. maenas;
RX MEDLINE=86232789; Pubmed=2872661;
RA Standler J., Dickson H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
CC PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 Y 1
DB 2 Y 2

RESULT 6
PSK_DAUCA STANDARD; PRT: 5 AA.
ID PSK_DAUCA
AC P58261;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHYTOSULFOKINE-ALPHA (PSK-ALPHA) [CONTAINS: PHYTOSULFOKINE-BETA (PSK-
BETA)].
OS Daucus carota (Carrot).
```

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:39:26 ; Search time 25.34 Seconds
(without alignments)
15,030 Million cell updates/sec

Title: US-09-281-760C-2
Perfect score: 18
Sequence: 1 YRXXL 5

Scoring table: BLOSUMP62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Minimum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	66.7	3	A22565	R-phycocerythrin a1
2	12	66.7	5	F22565	R-phycocerythrin ga
3	8	44.4	5	I40469	dnazx-like protein
4	7	38.9	3	A43391	TRH-like tripeptid
5	7	38.9	3	S68328	blood cell protein
6	7	38.9	4	A32039	tyrosine-melanocyt
7	7	38.9	4	A37832	phenol 2-monooxyge
8	7	38.9	4	S09478	globulin IV alpha
9	7	38.9	4	I61883	protamine PI - ora
10	7	38.9	4	PT0240	Ig heavy chain CRD
11	7	38.9	4	S43959	Ig mu chain V regi
12	7	38.9	4	I37013	protamine PI - Cer
13	7	38.9	4	I84439	protamine PI - sav
14	7	38.9	5	I HOROHA	proctolin - Americ
15	7	38.9	5	B37325	pap fimirial regul
16	7	38.9	5	I39964	ribosomal protein
17	7	38.9	5	I39966	ribosomal protein
18	7	38.9	5	I39965	ribosomal protein
19	7	38.9	5	E60274	major protein anti
20	7	38.9	5	PQ0009	angiotensin-conver
21	7	38.9	5	PQ0689	photosystem I 10.4
22	7	38.9	5	B61445	Leu-enkephalin - b
23	7	38.9	5	A61445	Met-enkephalin - b
24	7	38.9	5	A60411	proctolin - Atlant
25	7	38.9	5	PT0278	Ig heavy chain CRD
26	7	38.9	5	S68326	blood cell protein
27	7	27.8	3	PQ0010	angiotensin-conver
28	5	27.8	4	ECXAA	antho-Ramide neur
29	5	27.8	4	A02147	phagocytosis-stimu

30	5	27.8	4	2	ECNK	cardioexcitatory n
31	5	27.8	4	2	D41654	hypothetical prote
32	5	27.8	4	2	I40870	phospholipase C (E
33	5	27.8	4	2	J01273	neuropeptide Antho
34	5	27.8	4	2	A35779	neuropeptide Antho
35	5	27.8	4	2	A25844	antho-RF amide neu
36	5	27.8	4	2	A60418	FMRFamide - polych
37	5	27.8	4	2	PT0721	T-cell receptor be
38	5	27.8	4	2	S47552	ubiquitin - rat
39	5	27.8	5	2	JN0862	peptidyl-di-peptida
40	5	27.8	5	2	I40702	primase - Citrobac
41	5	27.8	5	2	A44955	alkanal monooxygen
42	5	27.8	5	2	D60274	major protein anti
43	5	27.8	5	2	B22565	R-phycocerythrin a1
44	5	27.8	5	2	T14910	hypothetical prote
45	5	27.8	5	2	A60803	neuropeptide - sea
46	5	27.8	5	2	S53595	hypothetical prote
47	5	27.8	5	2	PT0295	Ig heavy chain CRD
48	5	27.8	5	2	S62883	seminal plasma pro
49	5	27.8	5	2	PT0513	T-cell receptor be
50	5	27.8	5	2	PT0525	T-cell receptor be

ALIGNMENTS

RESULT 1
A22565
R-phycocerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 66.7%; Score 12; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YR 2
||
Db 2 YR 3

RESULT 2
F22565
R-phycocerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: F22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 66.7%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YR 2
||
Db 4 YR 5

RESULT 3

140469
 dmax-like protein - Bacillus subtilis (fragment)
 C:Species: Bacillus subtilis
 C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
 C:Accession: 140469
 R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
 Mol. Gen. Genet. 215, 478-482, 1989
 A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
 A:Reference number: 140469; MUID:89218958
 C:Accession: 140469
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <RES>
 A:Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204
 C:Genetics:
 A:Start codon: GTG

Query Match 44.4%; Score 8; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YR 2
 |:
 DB 3 Y0 4

RESULT 4

A43391
 TRH-like tripeptide - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: A43391
 R:Lackey, D.B.
 J. Biol. Chem. 267, 17508-17511, 1992
 A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-
 A:Reference number: A43391; MUID:92388092
 C:Accession: A43391
 A:Molecule type: protein
 A:Residues: 1-3 <LAC>
 C:Keywords: amidated carboxyl end; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 38.9%; Score 7; DB 2; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
 |:
 DB 2 Y 2

RESULT 5

S68328
 blood cell protein A - Molgula manhattensis (fragment)
 C:Species: Molgula manhattensis
 C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
 C:Accession: S68328
 R:Taylor, S.W.; Ross, M.M.; Waite, J.H.
 Arch. Biochem. Biophys. 324, 228-240, 1995
 A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th
 A:Reference number: S68325; MUID:96132650
 C:Accession: S68328
 A:Molecule type: protein
 A:Residues: 1-3 <TAI>

Query Match 38.9%; Score 7; DB 2; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
 |:
 DB 3 Y 3

RESULT 6

A32039
 tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
 C:Accession: A32039
 R:Horvath, A.; Kastin, A.J.
 J. Biol. Chem. 264, 2175-2179, 1989
 A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact
 A:Reference number: A32039; MUID:89123285
 C:Accession: A32039
 A:Molecule type: protein
 A:Residues: 1-4 <HOR>
 A:Experimental source: brain
 C:Superfamily: unassigned animal peptides
 C:Keywords: amidated carboxyl end
 F:4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 38.9%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
 |:
 DB 1 Y 1

RESULT 7

A37832
 phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (frag
 C:Species: Pseudomonas sp.
 C>Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993
 C:Accession: A37832
 R:Powlowaki, U.; Shingler, V.
 J. Bacteriol. 172, 6834-6840, 1990
 A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydro
 A:Reference number: A37832; MUID:91072231
 C:Accession: A37832
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <POW>
 C:Keywords: oxidoreductase

Query Match 38.9%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 Y 1
 |:
 DB 2 Y 2

RESULT 8

S09478
 globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
 N:Alternate names: 11S globulin alpha subunit gamma chain
 C:Species: Cucurbita sp. (cucurbit)
 C>Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
 C:Accession: S09478
 R:Omura, M.; Hara, I.; Matsubara, H.
 Plant Cell Physiol. 21, 157-167, 1980
 A:Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic a
 A:Reference number: S09466
 C:Accession: S09478

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:19:20 ; Search time 23.48 Seconds
(without alignments)
4.792 Million cell updates/sec

Title: US-09-281-760C-1
Perfect score: 18
Sequence: 1 LXXR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 16280

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
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3: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
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5: /cgn2_6/prodata/1/aa/PCPUS_COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	66.7	2	4	US-09-214-614-2
2	12	66.7	3	2	US-08-968-676-27
3	12	66.7	4	1	US-08-240-712-4
4	12	66.7	4	1	US-08-428-488-59
5	12	66.7	4	1	US-08-428-488-60
6	12	66.7	4	1	US-08-428-488-61
7	12	66.7	4	1	US-08-428-488-62
8	12	66.7	4	1	US-08-428-488-63
9	12	66.7	4	1	US-08-428-488-64
10	12	66.7	4	1	US-08-428-488-65
11	12	66.7	4	1	US-08-428-488-66
12	12	66.7	4	1	US-08-428-488-67
13	12	66.7	4	1	US-08-428-488-68
14	12	66.7	4	1	US-08-428-488-69
15	12	66.7	4	1	US-08-428-488-70
16	12	66.7	4	1	US-08-428-488-71
17	12	66.7	4	1	US-08-428-488-72
18	12	66.7	4	1	US-08-428-488-73
19	12	66.7	4	1	US-08-428-488-74
20	12	66.7	4	1	US-08-255-272-22
21	12	66.7	4	1	US-08-335-198-25
22	12	66.7	4	1	US-08-429-732-20
23	12	66.7	4	1	US-08-203-806B-15
24	12	66.7	4	1	US-08-443-890-4
25	12	66.7	4	1	US-08-706-178-2
26	12	66.7	4	2	US-08-441-871-1
27	12	66.7	4	2	US-08-441-871-63

28	12	66.7	4	2	US-08-441-871-65	Sequence 65, Appl
29	12	66.7	4	2	US-08-441-871-66	Sequence 66, Appl
30	12	66.7	4	2	US-08-441-871-68	Sequence 68, Appl
31	12	66.7	4	2	US-08-441-871-70	Sequence 70, Appl
32	12	66.7	4	2	US-08-473-022-2	Sequence 2, Appl
33	12	66.7	4	2	US-08-705-660-27	Sequence 27, Appl
34	12	66.7	4	2	US-08-705-660-28	Sequence 28, Appl
35	12	66.7	4	2	US-08-623-833B-61	Sequence 61, Appl
36	12	66.7	4	2	US-08-685-589A-6	Sequence 6, Appl
37	12	66.7	4	2	US-08-685-589A-62	Sequence 62, Appl
38	12	66.7	4	2	US-08-968-676-26	Sequence 26, Appl
39	12	66.7	4	2	US-08-752-844-12	Sequence 12, Appl
40	12	66.7	4	2	US-08-747-137-78	Sequence 78, Appl
41	12	66.7	4	2	US-08-591-196-12	Sequence 12, Appl
42	12	66.7	4	3	US-08-989-045-27	Sequence 27, Appl
43	12	66.7	4	3	US-08-989-045-28	Sequence 28, Appl
44	12	66.7	4	3	US-09-047-986B-20	Sequence 20, Appl
45	12	66.7	4	3	US-09-082-593-11	Sequence 11, Appl
46	12	66.7	4	4	US-09-058-562-4	Sequence 4, Appl
47	12	66.7	4	5	PCR-US92-09752-4	Sequence 4, Appl
48	12	66.7	4	5	PCR-US93-01669-16	Sequence 16, Appl
49	12	66.7	4	5	PCR-US96-08798-2	Sequence 2, Appl
50	12	66.7	4	6	5312899-1	Patent No. 5312899

ALIGNMENTS

RESULT 1
US-09-214-614-2
; Sequence 2, Application US/09214614
; Patent No. 6225100
; GENERAL INFORMATION:
; APPLICANT: Grund, Alan D.
; TITLE OF INVENTION: NOVEL ARYL SULFOTRANSFERASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/214,614
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 3161-15-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-214-614-2

Query Match 66.7%; Score 12; DB 4; length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YR 5
11
DB 1 YR 2

RESULT 2
US-08-968-676-27
Sequence 27, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-27

Query Match 66.7%; Score 12; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YR 5
11
DB 1 YR 2

RESULT 3
US-08-240-712-4
Sequence 4, Application US/08240712
Patent No. 5599907
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTONY JAMES
APPLICANT: STETLER, GARY L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
TITLE OF INVENTION: HEMOGLOBINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,712
FILING DATE: 09-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-712-4

Query Match 66.7%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YR 5
11
DB 3 YR 4

RESULT 4
US-08-428-488-59
Sequence 39, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:18:10 ; Search time 40.45 Seconds
(without alignments)
9.156 Million cell updates/sec

Title:	US-09-281-760C-1
Perfect score:	18
Sequence:	1 LXXR 5

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Total number of hits satisfying chosen parameter
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Maximum DB seq length: 0
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 50 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query								
No.	Score	Match	Length	DB	ID				Description
1	14	77.8	5	21	AAV69581				Generic immunogen
2	12	66.7	2	22	AAB91338				Opioid peptide SEQ
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4	12	66.7	3	19	AAW56224				Anti-inflammatory
5	12	66.7	3	22	AAB91597				Opioid peptide SEQ
6	12	66.7	4	5	AAV40467				Enkephalin analogu
7	12	66.7	4	6	AAV50336				Analgesic enkephal
8	12	66.7	4	6	AAV50680				Analgesic tetrapep
9	12	66.7	4	7	AAV61491				Analgesic peptide.
10	12	66.7	4	7	AAV61741				Analgesic peptide.
11	12	66.7	4	8	AAV71341				Analgesic peptide

12	66.7	4	8	AAP71580	Growth hormone rel
13	66.7	4	8	AAP71582	Growth hormone rel
12	66.7	4	8	AAP71581	Growth hormone rel
14	66.7	4	8	AAP71700	Analgesic peptide
15	66.7	4	13	AAR23084	Fluorinated peptide
16	66.7	4	13	AAR24410	CPase B-like enzyme
17	66.7	4	14	AAR41643	Internalisation si
18	66.7	4	14	AAR33660	Growth hormone rel
19	66.7	4	14	AAR33664	Growth hormone rel
20	66.7	4	14	AAR38136	Protease-non-1ab11
21	66.7	4	15	AAW51593	Peptide analogue #
22	66.7	4	15	AAW51589	Peptide analogue #
23	66.7	4	15	AAW51595	Peptide analogue #
24	66.7	4	15	AAR55498	Opitoid oligopeptid
25	66.7	4	15	AAR55497	Opitoid oligopeptid
26	66.7	4	15	AAR55502	Opitoid oligopeptid
27	66.7	4	15	AAR55503	Opitoid oligopeptid
28	66.7	4	15	AAR55506	Opitoid oligopeptid
29	66.7	4	15	AAR55507	Opitoid oligopeptid
30	66.7	4	15	AAR55481	Opitoid oligopeptid
31	66.7	4	15	AAR55484	Opitoid oligopeptid
32	66.7	4	15	AAR55485	Opitoid oligopeptid
33	66.7	4	15	AAR55488	Opitoid oligopeptid
34	66.7	4	15	AAR55489	Opitoid oligopeptid
35	66.7	4	15	AAR55493	Opitoid oligopeptid
36	66.7	4	15	AAR55494	Opitoid oligopeptid
37	66.7	4	15	AAR55465	Opitoid oligopeptid
38	66.7	4	15	AAR55467	Opitoid oligopeptid
39	66.7	4	15	AAR55469	Opitoid oligopeptid
40	66.7	4	15	AAR55471	Opitoid oligopeptid
41	66.7	4	15	AAR55473	Opitoid oligopeptid
42	66.7	4	15	AAR55475	Opitoid oligopeptid
43	66.7	4	15	AAR55477	Opitoid oligopeptid
44	66.7	4	15	AAR55479	Opitoid oligopeptid
45	66.7	4	15	AAR55449	Opitoid oligopeptid
46	66.7	4	15	AAR55451	Opitoid oligopeptid
47	66.7	4	15	AAR55452	Opitoid oligopeptid
48	66.7	4	15	AAR55455	Opitoid oligopeptid
49	66.7	4	15	AAR55433	Opitoid oligopeptid
50	66.7	4	15	AAR55435	Opitoid oligopeptid

ALIGNMENTS

RESULT

ID	standard; peptide; 5 AA.
AAV69581	

AC AAY69581;

DT 19-APR-2000 (first entry)

DE Generic immunogenic peptide SEQ ID NO:6, for anti-IgE Ab generation.

KW Immunogenic; autoimmunity; IGE autoantibody; immunoglobulin E; allergic rhinitis; probiotics; treatment

KW allergy; canine; prophylaxis; treatment.

OS Synthetic.

FH	key	Location/Qualifiers

FT /label= Xaa

Et

PN EP955311-A2.

PD 10-NOV-1999.

PF 09-APR-1999; 99EP-0107020.

PR	09-APR-1998;	98US-0058332.
PR	30-MAR-1999.	98US-00281761

XX

XX

PA (IDEX-) IDEX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-118182/11.

DR New peptides, useful for generating canine autoantibodies against

PT Immunoglobulin E (IgE) to treat allergic symptoms -

XX Claim 2; Page 5; 38pp: English.

CC Sequences AAY69576-Y69586 and AAY69598-Y69599 represent peptides that may
CC be used to induce anti-IgE (Immunoglobulin E) autoantibodies in a dog.
CC IgE is an important mediator of canine allergic responses, including type
CC I immediate hypersensitivity. It is estimated that up to 30% of all dogs
CC suffer from allergies or allergy-related skin disorders, and allergic
CC dermatitis is thought to affect between 3 and 15% of dogs. Common canine
CC allergens include fleas, pollens, moulds and dust, with flea allergy
CC being the most frequent. Once IgE has been released in response to
CC allergen, the IgE binds to receptors on mast cells. The IgE molecules
CC can then become cross-linked, which induces the mast cells to release
CC histamine, which leads to the manifestation of allergic symptoms. The
CC peptides of the invention correspond to epitopes of canine IgE, or
CC conservative variations thereof, that are accessible in circulating IgE
CC but not in IgE bound to mast cells. The autoantibodies produced on
CC immunisation with such peptides therefore target only circulating IgE,
CC avoiding the possibility that they may cross-link bound IgE molecules,
CC which would exacerbate an ongoing allergic response even in the absence
CC of allergen. Anti-IgE autoantibody induction results in an immune
CC response that targets the IgE-expressing B cell, which affects IgE
CC synthesis by downregulating IgE production by B cells and/or targeting
CC the IgE-producing B cell for destruction. The peptides of the invention
CC are therefore useful for the treatment or prophylaxis of allergic
CC symptoms in a dog.

CC Sequence 5 AA:

Query Match 77.8%; Score 14; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LXXR 5

DB 1 LXXR 5

RESULT 2

ID AAB91738 standard; Peptide; 2 AA.

AC AAB91738;

DT 22-JUN-2001 (first entry)

DE Opioid peptide SEQ ID NO:914.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy1; maleimido group; amino;
KW hydroxy1; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

XX Synthetic.

PM W0200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

DR Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure: Page 492; 733pp: English.

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy1 and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxy1/thiol groups on blood components to form a
CC peptide stable therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

CC Sequence 2 AA:

Query Match 66.7%; Score 12; DB 22; Length 2;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YR 5

DB 1 YR 2

RESULT 3

ID AAW33241 standard; peptide; 3 AA.

AC AAW33241;

DT 30-JAN-1998 (first entry)

DE Analgesic peptide.

KW Opioid receptor; treatment; prevention; pain; cancer; analgesic.

OS Synthetic.

KW Key Location/Qualifiers

FT Modified-site 1 /note= "HN=C(CH3)-Tyr"

FT Misc-difference 2 /note= "D-form residue"

FT Modified-site 3 /note= "Phe-N(CH3)-CH2-CH2-COOH"

PM W0910261-A1.

PD 20-MAR-1997.

PF 10-SEP-1996; 96WO-JP02572.

PR 11-SEP-1995; 95JP-0232161.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:38:16 ; Search time 37.83 Seconds
(without alignments)
19.333 Million cell updates/sec

Title: US-09-281-760C-1
Perfect score: 18
Sequence: 1 LXXYR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 8

Immun DB seq length: 0
Immun DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alt No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	4	Q08433	Q08433 rattus norv
2	3	16.7	5	P82070	P82070 litorea rub
3	3	16.7	5	P82071	P82071 litorea rub
4	3	16.7	5	P82072	P82072 litorea rub
5	3	16.7	5	P82073	P82073 litorea rub
6	3	16.7	5	P82099	P82099 litorea rub
7	3	16.7	5	P82100	P82100 litorea rub
8	2	11.1	5	Q99007	Q99007 hordeum vul

ALIGNMENTS

RESULT 1
ID Q08433
AC Q08433
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

PRELIMINARY: PRT: 4 AA.

DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOEAL (EC 2.4.1.17) (UDPGR)
DE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN.
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC - FUNCTION: UDPGR IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
ENDOGENOUS COMPOUNDS.
CC - CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC - BETA-D-GLUCURONOSIDE.
CC - SUBCELLULAR LOCATION: MICROSOME.
DR EMBL: S38636; AAR19259.1; -
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT 4 4
SQ SEQUENCE 4 AA: 473 MW; 633732C420000000 CRC64;

Query Match 22.2%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 L 1
Db 3 L 3

RESULT 2
ID P82070
AC P82070
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS litorea rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC litorea.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinhilber S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
TYLER M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
litorea rubella", the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC - FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC - TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC - MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA: 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
;

Db 3 F 3

RESULT 3

PRELIMINARY: PRT: 5 AA.

AC P82071: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA Steinboerner S.T., Maboitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella'; the skin peptide profile as a probe for the study of evolutionary trends of amphibians."
RT Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTI-BIOTIC ACTIVITY. SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- TISSUE SPECIFICITY: MM=626; METHOD=FAV.
CC -1- MASS SPECTROMETRY: MM=626; METHOD=FAV.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 Y 4
Db 3 F 3

RESULT 4

PRELIMINARY: PRT: 5 AA.

AC P82072: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE RUBELLIDIN 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA Steinboerner S.T., Maboitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians."
RT Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTI-BIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM=655; METHOD=FAV.
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 Y 4
Db 3 F 3

RESULT 5

PRELIMINARY: PRT: 5 AA.

AC P82073: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE RUBELLIDIN 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RA Maboitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog 'Litoria electrica'. Comparison with the skin peptides from Litoria rubella."
RT Aust. J. Chem. 52:0-0(1999).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTI-BIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 Y 4
Db 3 F 3

RESULT 6

PRELIMINARY: PRT: 5 AA.

AC P82099: 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE ELECTRIN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae; Litoria.
NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RA Maboitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog 'Litoria electrica'. Comparison with the skin peptides from Litoria rubella."
RT Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 16.7%; Score 3; DB 13; Length 5;

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:38:51 ; Search time 17.3 Seconds
(without alignments)
10.597 Million cell updates/sec

Title: US-09-281-760C-1
Perfect score: 18
Sequence: 1 LXXR 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 29

Minimum DB seq length: 0
Minimum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*Result No.	Score	Query Match Length	ID	Description
1	7	38.9	1 FAR3_HIRME	P42562 hirudo medi
2	7	38.9	2 FAR4_HIRME	P42563 hirudo medi
3	7	38.9	3 ALL4_CARMA	P81817 carcinus ma
4	7	38.9	4 FAR4_ARTTR	P41853 artiposchl
5	7	38.9	5 PRCR_PPRAM	P01373 periplaneta
6	7	38.9	6 PSK_DAUCA	P58261 daucus caro
7	5	27.8	7 FLRF_HIRME	P42561 hirudo medi
8	5	27.8	8 FMRF_MACNT	P01162 macrocallis
9	5	27.8	9 TURF_HUMAN	P01858 homo sapien
10	5	27.8	10 BIOB_SALTY	P12678 salmoneilla
11	5	27.8	11 UF01_MOUSE	P38639 mus musculu
12	4	22.2	12 GRWM_HUMAN	P01157 homo sapien
13	3	16.7	13 ACHI_ACHFU	P35904 achetina fu
14	3	16.7	14 PAP2_PARMA	P1864 pardachitus
15	3	16.7	15 SUGA_ACHDO	P19991 acheta dome
16	3	16.7	16 TPIS_CANFA	P54714 canis fami
17	3	16.7	17 UC22_MAIZE	P50628 zea mays (m
18	3	11.1	18 LUXE_VIBFI	P42722 vibrilo fisc
19	2	11.1	19 THYL_PIG	P01151 sus scrofa
20	2	11.1	20 DCML_PSECH	P19916 pseudomonas
21	2	11.1	21 DCMS_PSECH	P19918 pseudomonas
22	2	11.1	22 BIOA_CITFR	P13071 citrobacter
23	2	11.1	23 BIOA_SALTY	P12677 salmoneilla
24	2	11.1	24 BIOB_CITFR	P12997 citrobacter
25	2	11.1	25 BPP7_BOTIN	P30425 bothrops in
26	2	11.1	26 TRM3_ECOLI	P13973 escherichia
27	1	5.6	27 BOST_HUMAN	P02731 homo sapien
28	1	5.6	28 RM01_YEAST	P36515 saccharomyc
29	0	0.0	29 UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1
FAR3_HIRME STANDARD: PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
CC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:697-908(1991).
CC -i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 AA; 598 MW; 69D4073B30000000 CRC64;
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05; 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
DB 1 Y 1

RESULT 2
FAR4_HIRME STANDARD: PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
CC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:697-908(1991).
CC -i- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 AA; 616 MW; 69D4068B30000000 CRC64;
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+05; 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Y 4
DB 1 Y 1

RESULT 3
AL14_CARMA STANDARD: PRT; 5 AA.
ID AL14_CARMA
AC P81817;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUS MAENAS 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 NCBI_TaxId=6759;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation; Multigene family.
 KW MOD_RES 5
 FT AMIDATION (PEPTIDAL).
 SQ SEQUENCE 5 AA; 586 MW; 67287905AB300000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 Y 4
 DB 1 Y 1

RESULT 4
 FARP_ARTTR STANDARD; PRT; 5 AA.
 AC P41853;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFAMIDE-LIKE NEUROPEPTIDE RYIRF-AMIDE.
 OS Aripoosethia trianguata.
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
 OC Rhabdionphora; Seriate; Tricladida; Terricola; Geoplanidae;
 OC Arhundeidus.
 OX NCBI_TaxId=132421;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RX MEDLINE=94211927; PubMed=7909164;
 RA Maule A.G., Shaw G., Halton D.W., Curry W.J., Thim L.;
 RT "RIRFamide: a turbellarian FMRFamide-related peptide (FARP).";
 RL Regul. Pept. 50:37-43(1994).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 5
 FT AMIDATION.
 SQ SEQUENCE 5 AA; 754 MW; 69DA004B44600000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 Y 4
 DB 2 Y 2

RESULT 5
 ID PRT; PERAM STANDARD; PRT; 5 AA.
 AC P01373;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE PROCTOLIN.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 NCBI_TaxId=6978, 6850, 6759;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 RT in insects.";
 RL Life Sci. 17:1253-1256(1975).
 CC [2]
 CC BIOLOGICAL SOURCE.
 CC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron.";
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrov A.,
 RA Watson W.H., III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus.";
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86232789; PubMed=2872661;
 RA Standler J., Dickson H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, Carcinus maenas.";
 RL Peptides 7:67-72(1986).
 CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 CC PIR: A01644; HOROHA.
 DR PIR: A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 38.9%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 Y 4
 DB 2 Y 2

RESULT 6
 ID PSK_DAUCA STANDARD; PRT; 5 AA.
 AC PS6261;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PHYTOSULFOKINE-ALPHA (PSK-ALPHA) [CONTAINS: PHYTOSULFOKINE-BETA (PSK-
 DE BETA)].
 OS Daucus carota (Carrot).

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:32:30 ; Search time 25.34 Seconds
(without alignments)
15.030 Million cell updates/sec

Title: US-09-281-760C-1

Perfect score: 18

Sequence: 1 LXXYR 5

Scoring table: BIOSUM62

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Minimum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	66.7	3	2	A22565
2	12	66.7	5	2	F22565
3	8	44.4	4	2	I61883
4	8	44.4	4	2	I37013
5	8	44.4	4	2	I84439
6	8	44.4	5	2	B37325
7	8	44.4	5	2	I39964
8	8	44.4	5	2	I39965
9	8	44.4	5	2	I39965
10	8	44.4	5	2	I40469
11	7	38.9	3	2	A43391
12	7	38.9	3	2	S68328
13	7	38.9	4	2	A32039
14	7	38.9	4	2	A37832
15	7	38.9	4	2	S09478
16	7	38.9	4	2	PT0240
17	7	38.9	4	2	PT0240
18	7	38.9	4	2	S4959
19	7	38.9	5	2	H0808A
20	7	38.9	5	2	E60274
21	7	38.9	5	2	P00009
22	7	38.9	5	2	P00689
23	7	38.9	5	2	B61445
24	7	38.9	5	2	A60411
25	7	38.9	5	2	PT0278
26	7	38.9	5	2	S68326
27	7	38.9	5	4	A58728
28	5	27.8	3	2	P00010
29	5	27.8	4	1	ECXAA

30	5	27.8	4	2	A02147	phagocytosis-stimu
31	5	27.8	4	2	ECNK	cardioexcitatory n
32	5	27.8	4	2	D41654	hypothetical prote
33	5	27.8	4	2	I40870	phospholipase C (E
34	5	27.8	4	2	J01273	neuropeptide Antho
35	5	27.8	4	2	A35779	neuropeptide Antho
36	5	27.8	4	2	A25844	autho-RF amide neu
37	5	27.8	4	2	A60418	FMRFamide - polych
38	5	27.8	4	2	PT0721	T-cell receptor be
39	5	27.8	4	2	S47552	ubiquitin - rat
40	5	27.8	5	2	JN0862	peptidyl-dipeptida
41	5	27.8	5	2	I40702	primase - Citrobac
42	5	27.8	5	2	A44955	alkanal monooxyge
43	5	27.8	5	2	D60274	major protein anti
44	5	27.8	5	2	B22565	R-phycoerythrin al
45	5	27.8	5	2	T14910	hypothetical prote
46	5	27.8	5	2	A60803	neuropeptide - sea
47	5	27.8	5	2	S53595	hypothetical prote
48	5	27.8	5	2	PT0295	Ig heavy chain CRD
49	5	27.8	5	2	S62883	seminal plasma pro
50	5	27.8	5	2	PT0513	T-cell receptor be

ALIGNMENTS

RESULT 1
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85162601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 66.7%; Score 12; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YR 5
DB 2 YR 3

RESULT 2
F22565
R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85162601
A:Accession: F22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 66.7%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YR 5
DB 4 YR 5

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RESULT 3
161883
protamine P1 - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I61883
R:Queralto, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I61883
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12146; NID:938156; PIDN:CAA78130.1; PID:94379372

Query Match
44.4%; Score 8; DB 2; Length 4;
Best Local Similarity 25.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXY 4
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Db 1 MARY 4

RESULT 4
I37013
protamine P1 - Cercopithecus patas (fragment)
C:Species: Cercopithecus patas
C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I37013
R:Queralto, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I37013
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12150; NID:922814; PIDN:CAA78134.1; PID:94377415

Query Match
44.4%; Score 8; DB 2; Length 4;
Best Local Similarity 25.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXY 4
: |
Db 1 MARY 4

RESULT 5
I84439
protamine P1 - savannah baboon (fragment)
C:Species: Papio hamadryas doguera (savannah baboon)
C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I84439
R:Queralto, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I84439
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:Z12147; NID:938134; PIDN:CAA78131.1; PID:94379349

Query Match
44.4%; Score 8; DB 2; Length 4;
Best Local Similarity 25.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LXXY 4
: |
Db 1 MARY 4

RESULT 6
B37325
pap fibrial regulatory protein pap1 - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C:Accession: B37325
R:Braten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
J. Bacteriol. 173, 1789-1800, 1991
A:Title: Evidence for a methylaton-blocking factor (mbf) locus involved in pap pilus
A:Reference number: A37325; MUID:91154136
A:Accession: B37325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <BRA>
A:Cross-references: GB:M63747

Query Match
44.4%; Score 8; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXY 4
: |
Db 1 MARY 4

RESULT 7
I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsd regulatory target site.
A:Reference number: I39963; MUID:93015735
A:Accession: I39964
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:9143471
A:Gene: rpsd

Query Match
44.4%; Score 8; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXY 4
: |
Db 1 MARY 4

RESULT 8
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsd regulatory target site.
A:Reference number: I39963; MUID:93015735
A:Accession: I39966
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:51:47 ; Search time 12.9 Seconds
(without alignments)
19.189 Million cell updates/sec

Title: US-09-281-760C-5
Perfect score: 63
Sequence: 1 GNMUTYRRESK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 68711

Minimum DB seq length: 0
Minimum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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5: /cgn2_6/ptodata/1/1aa/PCYUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	44.4	11	2	US-08-486-839-12
2	28	44.4	11	3	US-09-151-011-12
3	28	44.4	11	4	US-09-343-623-12
4	26	41.3	8	1	US-08-014-426-16
5	26	41.3	8	1	US-08-014-426-39
6	26	41.3	8	5	PCT-US94-01319-16
7	26	41.3	8	5	PCT-US94-01319-39
8	25	39.7	8	4	US-09-082-593-11
9	25	39.7	8	1	US-08-014-426-17
10	25	39.7	8	1	US-08-014-426-23
11	25	39.7	8	1	US-08-014-426-38
12	25	39.7	8	5	PCT-US94-01319-17
13	25	39.7	8	5	PCT-US94-01319-23
14	25	39.7	8	5	PCT-US94-01319-38
15	24	38.1	6	2	US-08-482-228-127
16	24	38.1	6	3	US-08-482-528-127
17	24	38.1	8	1	US-08-014-426-29
18	24	38.1	8	4	US-08-444-818-566
19	24	38.1	8	4	US-08-444-818-567
20	24	38.1	9	5	PCT-US94-01319-29
21	24	38.1	9	2	US-08-725-736D-19
22	24	38.1	9	3	US-09-162-368B-19
23	24	38.1	9	4	US-09-161-877B-19
24	24	38.1	9	4	US-09-171-705-65
25	24	38.1	10	1	US-08-218-025A-122
26	24	38.1	10	1	US-08-218-025A-176
27	24	38.1	10	2	US-08-655-704B-2

28	24	38.1	10	3	US-09-107-755-2	Sequence 2, Appl
29	24	38.1	11	2	US-08-486-839-11	Sequence 11, Appl
30	24	38.1	11	3	US-09-151-011-11	Sequence 11, Appl
31	24	38.1	11	4	US-09-343-623-11	Sequence 11, Appl
32	23	36.5	6	1	US-08-487-006-17	Sequence 17, Appl
33	23	36.5	6	1	US-08-209-261B-6	Sequence 6, Appl
34	23	36.5	6	2	US-08-317-310A-19	Sequence 19, Appl
35	23	36.5	6	2	US-08-486-659A-17	Sequence 17, Appl
36	23	36.5	6	5	PCT-US95-13041-19	Sequence 19, Appl
37	23	36.5	7	1	US-08-230-473-2	Sequence 21, Appl
38	23	36.5	8	1	US-08-014-426-21	Sequence 28, Appl
39	23	36.5	8	1	US-08-014-426-28	Sequence 36, Appl
40	23	36.5	8	1	US-08-014-426-36	Sequence 37, Appl
41	23	36.5	8	1	US-08-014-426-37	Sequence 11, Appl
42	23	36.5	8	1	US-08-403-634-11	Sequence 14, Appl
43	23	36.5	8	1	US-08-403-634-14	Sequence 162, Appl
44	23	36.5	8	1	US-08-189-331-162	Sequence 163, App
45	23	36.5	8	1	US-08-189-331-163	Sequence 163, App
46	23	36.5	8	2	US-08-471-068-163	Sequence 163, App
47	23	36.5	8	2	US-08-471-068-163	Sequence 14, Appl
48	23	36.5	8	4	US-08-913-441B-11	Sequence 14, Appl
49	23	36.5	8	4	US-08-913-441B-14	Sequence 7, Appl
50	23	36.5	8	4	US-09-026-904-7	

ALIGNMENTS

RESULT 1
US-08-486-839-12
; Sequence 12, Application US/08486839
; Patent No. 5928928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for decomposing chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486, 839
; FILING DATE: 07 - June - 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; US-08-486-839-12
Query Match 44.4%, Score 28; DB 2; Length 11;

Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GNM/LTW 6
1:1111
DB 3 GNL/DW 8

RESULT 2

US-09-151-011-12
Sequence 12, Application US/09151011
Patent No. 6057142

GENERAL INFORMATION:

APPLICANT:
TITLE OR INVENTION: A Human Chitinase, Its Recombinant
TITLE OR INVENTION: Production, Its Use For Decomposing Chitin, Its Use In
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 6900 Jericho Turnpike
CITY: Syosset
STATE: New York
COUNTRY: United States of America
ZIP: 11791

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151_011
FILING DATE: 10 September - 1998
ATTORNEY/AGENT INFORMATION:
NAME: Morris, Robert C.
REGISTRATION/DOCKET NUMBER: 42,910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO

US-09-151-011-12

Query Match 44.4%; Score 28; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GNM/LTW 6
1:1111
DB 3 GNL/DW 8

RESULT 3

US-09-343-623-12

Sequence 12, Application US/09343623
Patent No. 6303118

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: A human chitinase, its recombinant

TITLE OF INVENTION: production, its use for decomposing chitin, its use

TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann & Baron

STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/343,623

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/486,839

FILING DATE: 07-June-1995

ATTORNEY/AGENT INFORMATION:

NAME: Baron, Ronald J.

REGISTRATION/DOCKET NUMBER: 29,281

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 822-3550

TELEFAX: (516) 822-3582

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-09-343-623-12

Query Match 44.4%; Score 28; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GNM/LTW 6
1:1111
DB 3 GNL/DW 8

RESULT 4

US-08-014-426-16

Sequence 16, Application US/08014426
Patent No. 5512435

GENERAL INFORMATION:

APPLICANT: Renschler, Markus F.

APPLICANT: Levy, Ronald

APPLICANT: Bhatt, Ramesh

TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE

TITLE OF INVENTION: PEPTIDES

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/014,426

FILING DATE: 05-FEB-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:55:15 ; Search time 25.77 Seconds
(without alignments)
62.437 Million cell updates/sec

Title: US-09-281-760C-5
Perfect score: 63

Sequence: 1 GNMJMYRESK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 1277

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	25	39.7	9	4	Q9UWAO
2	25	39.7	9	12	Q85723
3	22	34.9	9	4	Q9UC36
4	20	31.7	11	7	Q77893
5	19	30.2	8	8	Q9TDM2
6	18	28.6	8	2	Q9R9C2
7	18	28.6	9	4	Q16386
8	18	28.6	9	4	Q9UK44
9	18	28.6	9	4	Q9BYF9
10	18	28.6	10	4	Q15342
11	18	28.6	10	8	Q9MJO5
12	18	28.6	10	13	P82080
13	18	28.6	11	13	Q90735
14	17.5	27.8	10	8	P92771
15	17	27.0	9	5	P82003
16	17	27.0	10	4	Q9UJ48
17	17	27.0	10	5	Q26093
18	17	27.0	10	12	Q88082
19	17	27.0	11	4	Q9UE69

20	16.5	26.2	10	8	Q79891	Q79891	crocaplytus
21	16.5	26.2	10	8	Q79894	Q79894	gambella w1
22	16.5	26.2	10	8	Q79909	Q79909	sauromalus
23	16.5	26.2	10	8	Q92YV3	Q92YV3	disposaurus
24	16.5	26.2	10	8	Q9T8G5	Q9T8G5	liolaemus o
25	16.5	26.2	10	8	Q9VRD2	Q9VRD2	dirosophila
26	16.5	26.2	10	8	Q9VVD3	Q9VVD3	rattus sp.
27	16.5	26.2	10	8	Q9R635	Q9R635	chlamydia t
28	16.5	26.2	10	8	Q9M43	Q9M43	homo sapien
29	16.5	26.2	10	12	Q82622	Q82622	avian infec
30	16.5	26.2	10	2	Q54217	Q54217	staphylococ
31	16.5	26.2	10	4	Q9UCU6	Q9UCU6	homo sapien
32	16.5	26.2	10	10	P82443	P82443	nicotiana t
33	16.5	26.2	10	7	Q9UX7	Q9UX7	homo sapien
34	15.5	24.6	10	8	Q92616	Q92616	cnemidophor
35	15.5	24.6	10	8	Q9T698	Q9T698	shinisaurus
36	15.5	23.8	7	13	P82065	P82065	illoria rub
37	15.5	23.8	8	4	Q9UMH9	Q9UMH9	homo sapien
38	15.5	23.8	8	4	Q9UT50	Q9UT50	homo sapien
39	15.5	23.8	8	11	Q62721	Q62721	rattus norv
40	15.5	23.8	10	6	Q9TU33	Q9TU33	canis famil
41	15.5	23.8	10	8	P92576	P92576	bipes bipor
42	15.5	23.8	10	8	P92632	P92632	eremias gra
43	15.5	23.8	10	11	Q9R020	Q9R020	mus muscula
44	15.5	23.8	10	13	Q9PR09	Q9PR09	sparus aura
45	15.5	23.8	11	2	Q47345	Q47345	escherichia
46	15.5	23.8	11	7	Q77892	Q77892	oreochromis
47	15.5	23.8	11	7	Q77899	Q77899	oreochromis
48	15.5	23.8	11	7	Q77900	Q77900	oreochromis
49	15.5	23.8	11	7	Q77901	Q77901	oreochromis
50	15.5	23.8	11	7	Q77902	Q77902	oreochromis

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	Q9UWAO	PRELIMINARY; PRT; 9 AA.
AC	Q9UWAO	
DT	01-MAY-2000 (TREMURBL. 13, Created)	
DT	01-MAY-2000 (TREMURBL. 13, Last sequence update)	
DT	01-MAY-2000 (TREMURBL. 13, Last annotation update)	
DE	KIT PROTEIN (FRAGMENT).	
GN	KIT.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=94061059; PubMed=7694728;	
RA	Spitz R.A., Holmes S.A., Berg S.Z., Nordlund J.J., Fukai K.;	
RT	"A recurrent deletion in the KIT (mast/stem cell growth factor	
RT	receptor) proto-oncogene is a frequent cause of human piebaldism."	
RL	Hum. Mol. Genet. 2:1499-1500(1993).	
DR	EMBL; S67686; AAD13996.1; -	
FT	NON TER	
SO	SEQUENCE	
	9 AA; 1182 MW; 0BC504032361B5AB CRC64;	

Query Match 39.7% Score 25; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.7e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	5 TWYRES 10
DB	4 TWKREN 9
RESULT	2
Q85723	PRELIMINARY; PRT; 9 AA.
ID	Q85723

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AC 085723;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, last annotation update)
DE SIS ONCOGENE (FRAGMENT).
OS Simian sarcoma virus.
OC Viruses: Retroid viruses; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11817;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84106822; PubMed=6319011;
RA Devare S.G., Shatzman A.R., Robbins K.C., Rosenberg M., Aaronson S.A.;
RT "Expression of the PDGF-related transforming protein of simian Sarcoma
RT Cell 36:13-19(1984);
DI EMBL_K01473; AAA46816.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1048 MW; 9C53A866C361A731 CRC64;

Query Match
Best Local Similarity 39.7%; Score 25; DB 12; Length 9;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MNTW 6
DB 1 MNTW 5

RESULT 3
ID 09UC36 PRELIMINARY; PRT; 9 AA.
AC 09UC36;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE 28 KDA HEAT SHOCK PROTEIN HOMOLOG FRAGMENT 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shinozawa H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Computerization of small heat shock protein with alpha B crystallin
RT from human skeletal muscle.";
DI EMBL_J01011; AF092421; AA03041.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F7B43 CRC64;

Query Match
Best Local Similarity 34.9%; Score 22; DB 4; Length 9;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 WYRSK 11
DB 2 WYRSK 7

RESULT 4
ID 077893 PRELIMINARY; PRT; 11 AA.
AC 077893;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
DE MHC CLASS II B LOCUS 10 (FRAGMENT).
OS Oreoichthys niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreoichthys.

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OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., McAndrew B., Vincek V., Zaleska-Rutczynska Z.,
RA Szeleman H., Figueroa F., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci";
DI EMBL_AF050003; AAC41342.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 11 AA; 1296 MW; 68775B73786B572B CRC64;

Query Match
Best Local Similarity 31.7%; Score 20; DB 7; Length 11;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 WYRE 9
DB 1 WYRE 4

RESULT 5
ID 09TD02 PRELIMINARY; PRT; 8 AA.
AC 09TD02;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
OS Terranatos dolichopterus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Terranatos.
OX NCBI_TaxID=61836;
RN [1]
RP SEQUENCE FROM N.A.
RA Hrbek T., Larson A.;
RT "The evolution of diapause in the killifish family Rivulidae
RT (Atherinomorpha, Cyprinodontiformes): A molecular phylogenetic and
RT biogeographic perspective.";
DI EMBL_AF092421; AA03041.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 1084 MW; F0C9D3640DDA4056 CRC64;

Query Match
Best Local Similarity 30.2%; Score 19; DB 8; Length 8;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 MNTWY 7
DB 2 INARWF 7

RESULT 6
ID 09R9C2 PRELIMINARY; PRT; 8 AA.
AC 09R9C2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DE PLASMID CP32-3, POSSIBLE PARTITION PROTEINS, COMPLETE CDS (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid CP32-3.
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:56:21 ; Search time 10.33 Seconds

(without alignments)
39.043 Million cell updates/sec

Title: US-09-281-760C-5

Perfect score: 63

Sequence: 1 GMLTWRRESK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 388

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	41.3	10	1	APE_CAPGI
2	19	30.2	10	1	UPA9_HUMAN
3	18	28.6	10	1	GON2_CHICK
4	17	27.0	8	1	UPA9_HUMAN
5	16	25.4	9	1	HUTU_KLEAE
6	16	25.4	9	1	LMIP_LOCOMI
7	15	23.8	9	1	FARF_CALSI
8	15	23.8	9	1	NEF_HVIZ8
9	15	23.8	10	1	GON1_PETMA
10	14	22.2	10	1	PNEU_RAT
11	14	22.2	10	1	RL16_ACHLA
12	14	22.2	10	1	URE3_MORMO
13	14	22.2	10	1	UXA6_CHLTR
14	13.5	21.4	8	1	LCK3_LEUMA
15	13	20.6	8	1	ACL_THUAL
16	13	20.6	8	1	PLP_BRANA
17	13	20.6	10	1	BPP2_BOTUA
18	13	20.6	10	1	GON3_PETMA
19	13	20.6	10	1	LABA_JATMU
20	13	20.6	10	1	TOPI_SALTY
21	13	20.6	11	1	LPM_THEST
22	13	20.6	11	1	TKN2_UPEBU
23	12	19.0	6	1	LOK1_LOCOMI
24	12	19.0	7	1	IGNO_DACDE
25	12	19.0	7	1	WMA2_ACHFU
26	12	19.0	7	1	WMA2_ACHFU
27	12	19.0	8	1	AKH_LIBAU
28	12	19.0	8	1	LCK1_LEUMA
29	12	19.0	8	1	LCK2_LEUMA
30	12	19.0	8	1	LCK4_LEUMA
31	12	19.0	8	1	LCK5_LEUMA
32	12	19.0	8	1	LCK6_LEUMA
33	12	19.0	8	1	LCK7_LEUMA

34	12	19.0	8	1	LCK8_LEUMA	P19990 leucophaea
35	12	19.0	9	1	UHA2_HUMAN	P40929 homo sapien
36	12	19.0	10	1	AKHX_LOCOMI	P81626 locusta mig
37	12	19.0	10	1	COXO_RAT	P80432 rattus norv
38	12	19.0	10	1	HTE1_ROMAT	P18110 romalea mic
39	12	19.0	10	1	NO40_TOBAC	P55962 nicotiana t
40	12	19.0	10	1	SYK_CAMUP	O46464 campylobact
41	12	19.0	10	1	TKU1_UREUN	P40751 urechis uni
42	12	19.0	11	1	CEPI_ACHFU	P22790 achetina fu
43	12	19.0	11	1	ULAG_HUMAN	P31933 homo sapien
44	11	17.5	5	1	BPP1_BOTIN	P30425 bothriops in
45	11	17.5	5	1	UP01_MOUSE	P38639 mus musculu
46	11	17.5	7	1	WMA3_ACHFU	P35921 achetina fu
47	11	17.5	8	1	AKHE_GRYBT	P14086 gryllus bim
48	11	17.5	8	1	AKH_MEIML	P25423 melolontha
49	11	17.5	8	1	AKH_TABAT	P14595 tabanus atr
50	11	17.5	8	1	AL15_CALVO	P41841 calliphora

ALIGNMENTS

RESULT	1	STANDARD	PRT	10 AA.
AC	APE_CAPGI			
AC	P80474;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-OCT-1996 (Rel. 34, Last annotation update)			
DE	AMINOPEPTIDASE (EC 3.4.11.-) (FRAGMENT).			
OS	Capnocytophaga gingivalis.			
OC	Bacteria; CF8 group; Flavobacteria; Flavobacteriaceae; Capnocytophaga.			
OX	NCBI_TaxID=101/;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=ATCC 33624;			
RX	MEDLINE=96118234; PubMed=8574402;			
RA	Spratt D.A., Greenman J., Schaffer A.G.;			
RT	"Capnocytophaga gingivalis aminopeptidase: a potential virulence factor."			
RL	Microbiology 141:3087-3093(1995).			
CC	- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.			
CC	OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL CAVITY.			
CC	- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.			
KW	Hydrolase; Aminopeptidase; Magnesium; Calcium.			
FT	NON_TER 1			
FT	NON_TER 10			
SO	SEQUENCE 10 AA; 1306 MW; 00C0A6DBA3772694 CRC64;			

Query Match 41.3%; Score 26; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 54;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY	2 MNLTWY 7			
QY	: : : :			
Db	2 VNMMLY 7			
RESULT	2			
ID	UPA9_HUMAN	STANDARD;	PRT;	10 AA.
AC	P30095;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 35) (FRAGMENT).			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

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OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Rivier F., Pasquall C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RT Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.2, ITS MW IS: 15 KDA.
DR SWISS-2DPAGE: P30095; HUMAN.
FT NON_TER 1 1
FT SEQUENCE 10 AA: 1233 MW; 37AD72B409C681B7 CRC64;
SO

Query Match 30.2%; Score 19; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 9e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 NUTWYRESK 11
DB 2 NPTWFRDNE 10

RESULT 3
GON2_CHICK STANDARD: PRT; 10 AA.
ID GON2_CHICK AC P37043; P20408; P81750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GONADOTROPIN II (GONADOTROPIN-RELEASING HORMONE II) (GNRH-II)
DE (LH-RH II) (LULIBERIN II).
OS Gallus gallus (Chicken).
OS Alligator mississippiensis (American alligator),
OS Squallus acanthias (Spiny dogfish), and
OS Hydroloagus colliet (Spotted ratfish) (Pacific ratfish);
OS Clupea pallasi (Pacific herring);
OS Euhryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CC NCBI_TaxID=9031, 8496, 7797, 7873, 30724;
OK NCBI_TaxID=9031, 8496, 7797, 7873, 30724;
RN [1]
RP SEQUENCE.
RC SPECIES=chicken; TISSUE=Hypothalamus;
RX MEDLINE=8422059; PubMed=6427779;
RA Miyamoto K., Hasegawa Y., Nomura M., Igarashi M., Kangawa K.,
RA Matsuo H.;
RT "Identification of the second gonadotropin-releasing hormone in
RT chicken hypothalamus: evidence that gonadotropin secretion is
RT probably controlled by two distinct gonadotropin-releasing hormones
RT in avian species.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3874-3878(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=A. mississippiensis; TISSUE=Brain;
RX MEDLINE=9152338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRoy J.E., Park M.,
RA Lancel V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
RN [3]
RP SEQUENCE.
RC SPECIES=S. acanthias; TISSUE=Brain;
RX MEDLINE=9235300; PubMed=1631133;
RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
RA Naboriak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
RT "Distinct sequence of gonadotropin-releasing hormone (GNRH) 1a
RT dogfish brain provides insight into GNRH evolution.";
RN [4]
RP SEQUENCE.
RC SPECIES=H. colliet; TISSUE=Brain;
RX MEDLINE=91340067; PubMed=1678723;
RA Lovejoy D.A., Sherwood N.M., Fischer W.H., Jackson B.C., Rivier J.E.,
RA Lee T.;
RT "Primary structure of gonadotropin-releasing hormone from the brain
RT of a holocarpal (ratfish: Hydroloagus colliet).";
RL Gen. Comp. Endocrinol. 82:152-161(1991).
RN [5]
RP SEQUENCE. AND FUNCTION.
RC SPECIES=C. pallasi; TISSUE=Brain, and Pituitary;
RX MEDLINE=20114351; PubMed=10650929;
RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA Chang J.P., Rivier J.E., Sherwood N.M.;
RT "Primary structure and function of three gonadotropin-releasing
RT hormones, including a novel form, from an ancient teleost, herring.";
RT hormones, including a novel form, from an ancient teleost, herring.";
RL Endocrinology 141:505-512(2000).
CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR PIR: B60066; RHA02.
DR PIR: A61126; A61126.
DR PIR: B46030; B46030.
DR InterPro: IPR002012; GNRH.
DR Pfam: PF00446; GNRH; 1.
DR Prosite: PS00473; GNRH; 1.
KM Hormone; Amidation; Hypothalamus.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
FT SEQUENCE 10 AA: 1254 MW; 284B2E43781F5A3 CRC64;
SO

Query Match 28.6%; Score 18; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 WY 7
DB 7 WY 8

RESULT 4
UPAA_HUMAN STANDARD: PRT; 8 AA.
ID UPAA_HUMAN AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 36) (FRAGMENT).
OS Homo sapiens (human); Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC NCBI_TaxID=9606;
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Rivier F., Pasquall C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RT Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 KDA.
DR SWISS-2DPAGE: P30096; HUMAN.
FT NON_TER 1 1
FT SEQUENCE 8 AA: 909 MW; 86677B59D1A72042 CRC64;
SO

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:54:10 ; Search time 19.63 Seconds
(without alignments)
42.686 Million cell updates/sec

Title: US-09-281-760C-5
Perfect score: 63
Sequence: 1 GNNLTWYRESK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 1324

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR_68:*

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	39.7	7	2	PN0649
2	23	36.5	11	2	A33571
3	21	30.2	10	2	F49033
4	19	30.2	10	2	C54226
5	18	28.6	7	2	S21230
6	18	28.6	9	2	A61230
7	18	28.6	9	2	S78426
8	18	28.6	10	1	RHA02
9	18	28.6	10	1	A61126
10	18	28.6	10	2	B46030
11	18	28.6	10	2	PT0291
12	18	28.6	11	2	PT0310
13	18	28.6	11	2	PT0302
14	17.5	27.8	10	2	T14219
15	17	27.0	10	2	F60589
16	17	27.0	10	2	B38887
17	16.5	26.2	10	2	T17057
18	16.5	26.2	10	2	T12303
19	16.5	26.2	10	2	T17060
20	16.5	26.2	10	2	T17072
21	16	25.4	9	1	AKLQIM
22	16	25.4	9	2	C36730
23	16	25.4	9	2	PT0272
24	16	25.4	10	2	H60787
25	16	25.4	10	2	D60788
26	16	25.4	10	2	B60787
27	16	25.4	10	2	A60788
28	16	25.4	10	2	G60527
29	16	25.4	10	2	C60589

30	16	25.4	10	2	D60588	sperm-activating p
31	16	25.4	11	2	C53652	thir protein - pse
32	16	25.4	11	2	JQ2307	hypothetical 1.5K
33	16	25.4	11	2	JQ2317	hypothetical 1.5K
34	16	25.4	11	2	A29806	acidic proline-ric
35	16	25.4	11	2	A49037	TCR gamma V-J regl
36	15.5	24.6	10	2	T13976	cytochrome-c oxida
37	15	23.8	5	2	F22565	R-phycocerythrin ga
38	15	23.8	5	2	A60803	neuropeptide - sea
39	15	23.8	7	2	PX0008	glucuronosyltransf
40	15	23.8	9	2	S55696	phosphoenolpyruvat
41	15	23.8	10	1	RHLMGS	gonadoliberin - se
42	15	23.8	10	2	A47593	mercury resistance
43	15	23.8	10	2	PC2172	triacylglycerol 11
44	15	23.8	10	2	G60589	sperm-activating p
45	15	23.8	10	2	A60589	sperm-activating p
46	15	23.8	10	2	B39308	glycine reductase
47	15	23.8	10	2	PT0289	Ig heavy chain CRD
48	15	23.8	10	2	PH0923	T-cell receptor be
49	15	23.8	10	2	T13838	cytochrome-c oxida
50	15	23.8	10	2	T14019	cytochrome-c oxida

ALIGNMENTS

RESULT 1
PN0649
alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (f
C:Species: Bacillus sp.
C:Date: 19-May-1994 #sequence-revision 19-May-1994 #text-change 07-May-1999
C:Accession: PN0649
R:Kim, C.H.; Choi, H.I.; Lee, D.S.
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
A:Title: Purification and biochemical properties of an alkaline pullulanase from alka
A:Reference number: PN0649; MWID:94080025
A:Accession: PN0649
A:Molecule type: protein
A:Residues: 1-7 <KIM>
C:Comment: This enzyme is used together with glucosylase to improve the efficiency of
nient in high maltose syrups.
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 39.7%; Score 25; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.2e+05;
Matches 2; Conservative. 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 MNLWY 7
DB 2 LNMSWF 7

RESULT 2
A33571
folliculin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 09-Mar-1990 #sequence-revision 09-Mar-1990 #text-change 30-Sep-1993
C:Accession: A33571
R:Gospodarowicz, D.; Lau, K.
Biochem. Biophys. Res. Commun. 165, 292-298, 1989
A:Title: Plutitary follicular cells secrete both vascular endothelial growth factor a
A:Reference number: A33571; MWID:90073725
A:Accession: A33571
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <GOS>

Query Match 36.5%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 WYRESK 11
| | | | |
Db 4 WYROAK 9

RESULT 3

T-cell receptor gamma chain V-D-J region - human (fragment)
F49033
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: F49033
R:Korita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Burr, J. Immunol. 21, 2939-3007, 1991.
A:Title: Functionally distinct subsets of human gamma/delta T cells.
A:Reference number: A49033; MUID:92083926
A:Accession: F49033
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <MOR>
A:Cross-references: GB:S72605; NID:9240700; PIDN:AB20632.1; PID:9240701
A:Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIPI:72605)
C:Keywords: T-cell receptor

Query Match 33.3%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 WYRE 9
| | | | |
Db 7 WYKK 10

RESULT 4

Light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)
C54226
C:Species: Chromatium purpuratum
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C:Accession: C54226
R:Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.
Biochemistry 33, 2178-2184, 1994.
A:Title: Purification and characterization of the peripheral antenna of the purple-sulfur
A:Reference number: A54226; MUID:94162224
A:Accession: C54226
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <KEK>
C:Keywords: antenna complex; light-harvesting polypeptide

Query Match 30.2%; Score 19; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 RESK 11
| | | | |
Db 1 RESK 4

RESULT 5

dermorphin (Tyr-4, Asn-7) [validated] - two-colored leaf frog (fragment)
S21230
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C:Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C:Accession: S21230
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992.
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:93335502
A:Accession: S21230
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MG>

C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 28.6%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 WY 7
| | | | |
Db / 4 WY 5

RESULT 6

calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)
A61230
N:Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; lamin
C:Species: Rana pipiens (northern leopard frog)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C:Accession: A61230
R:McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991.
A:Title: Frog cardiac calsequestrin. Identification, characterization, and subcellula
rdium.
A:Reference number: A61230; MUID:91316784
A:Accession: A61230
A:Molecule type: protein
A:Residues: 1-9 <MCU>
C:Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding pro
C:Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound t
C:Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in
C:Superfamily: calsequestrin
C:Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; ske

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GNNLTWY 7
| | | | |
Db 3 GINPEPY 9

RESULT 7

52.5K protein - spiny lobster (fragment)
S78426
C:Species: Panulirus argus (spiny lobster)
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 19-May-2000
C:Accession: S78426
R:James, M.O.; Boyle, S.M.; Tripathi-Rosenthal, H.G.; Smith, W.C.; Greenberg, R.M.; Sh
Archi. Biochem. Biophys. 329, 31-38, 1996.
A:Title: CDKs and protein sequence of a major form of P450, CYP2L, in the hepatopan
A:Reference number: S68856; MUID:96201120
A:Accession: S78426
A:Molecule type: protein
A:Residues: 1-9 <JAM>
A:Experimental source: hepatopancreas microsomes

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 TWYRE 9
| | | | |
Db 1 TWIKK 5

RESULT 8

gonadotropin-releasing hormone II - American alligator
RH02
N:Alternate names: gonadotropin-releasing hormone II
C:Species: Alligator mississippiensis (American alligator)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:48:46 ; Search time 12.88 Seconds
(without alignments)
12.230 Million cell updates/sec

Title: US-09-281-760C-4

Perfect score: 35

Sequence: 1 TLEFYR 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 35098

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA.*
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5: /cgn2-6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2-6/ptodata/1/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	62.9	7	4	US-09-258-754-22	Sequence 22, Appl
2	22	62.9	7	4	US-09-042-107-22	Sequence 22, Appl
3	20	57.1	7	1	US-08-105-416-36	Sequence 36, Appl
4	20	57.1	7	2	US-08-473-656A-36	Sequence 36, Appl
5	18	51.4	5	4	US-09-020-880-78	Sequence 78, Appl
6	18	51.4	7	2	US-08-437-116A-11	Sequence 11, Appl
7	18	51.4	7	2	US-08-530-792D-11	Sequence 11, Appl
8	17	48.6	3	2	US-08-968-676-27	Sequence 27, Appl
9	17	48.6	4	2	US-08-968-676-26	Sequence 26, Appl
10	17	48.6	5	2	US-08-968-676-25	Sequence 25, Appl
11	17	48.6	5	4	US-09-020-880-75	Sequence 75, Appl
12	17	48.6	6	1	US-08-166-930-1	Sequence 1, Appl
13	17	48.6	6	2	US-08-968-676-24	Sequence 24, Appl
14	17	48.6	6	2	US-08-727-045A-1	Sequence 1, Appl
15	17	48.6	6	6	5472855-18	Patent No. 5472855
16	17	48.6	7	1	US-08-335-198-12	Sequence 12, Appl
17	17	48.6	7	2	US-08-968-676-22	Sequence 22, Appl
18	17	48.6	7	4	US-09-258-754-22	Sequence 22, Appl
19	17	48.6	7	4	US-09-042-107-21	Sequence 21, App
20	16	45.7	6	1	US-08-789-333F-77	Sequence 77, Appl
21	16	45.7	6	1	US-08-519-103-4	Sequence 4, Appl
22	16	45.7	6	2	US-08-204-417A-4	Sequence 4, Appl
23	16	45.7	6	2	US-08-177-109A-8	Sequence 8, Appl
24	16	45.7	6	2	US-08-177-109A-8	Sequence 8, Appl
25	16	45.7	6	2	US-08-687-706-8	Sequence 8, Appl
26	16	45.7	6	2	US-08-687-706-8	Sequence 8, Appl
27	16	45.7	6	2	US-08-687-706-38	Sequence 38, Appl

28	16	45.7	6	4	US-09-018-635-4	Sequence 4, Appl
29	16	45.7	7	1	US-08-401-512-74	Sequence 74, Appl
30	16	45.7	7	1	US-08-401-512-76	Sequence 76, Appl
31	16	45.7	7	1	US-08-264-093-25	Sequence 25, Appl
32	16	45.7	7	1	US-08-346-333-84	Sequence 84, Appl
33	16	45.7	7	1	US-08-290-301-81	Sequence 81, Appl
34	16	45.7	7	3	US-09-188-579-105	Sequence 105, App
35	16	45.7	7	4	US-09-273-565-60	Sequence 60, Appl
36	16	45.7	7	4	US-09-226-012-109	Sequence 109, App
37	16	45.7	7	4	US-09-226-012-111	Sequence 111, Appl
38	16	45.7	7	4	US-09-475-316A-43	Sequence 43, Appl
39	16	45.7	7	4	US-09-315-444-105	Sequence 105, App
40	16	45.7	7	5	PCN-US91-07506-84	Sequence 84, Appl
41	15	42.9	5	1	US-08-313-0758-22	Sequence 22, Appl
42	15	42.9	5	1	US-08-460-343B-47	Sequence 47, Appl
43	15	42.9	5	1	US-08-398-028B-47	Sequence 47, Appl
44	15	42.9	5	2	US-08-504-265B-47	Sequence 47, Appl
45	15	42.9	5	3	US-09-130-663-7	Sequence 7, Appl
46	15	42.9	5	3	US-08-649-100-19	Sequence 19, Appl
47	15	42.9	5	3	US-08-649-100-35	Sequence 35, Appl
48	15	42.9	5	4	US-09-020-880-80	Sequence 80, Appl
49	15	42.9	5	4	US-09-203-623-22	Sequence 22, Appl
50	15	42.9	5	4	US-09-432-333-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-258-754-22
; Sequence 22, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; EARLIER FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-22

Query Match      62.9%; Score 22; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 TLEFYR 6
DB      2 SLEFYR 7

RESULT 2
US-09-042-107-22
; Sequence 22, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
```

;; CURRENT APPLICATION NUMBER: US/09/042,107
;; CURRENT FILING DATE: 1998-03-13
;; NUMBER OF SEQ ID NOS: 436
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO: 22
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE: Artificial Sequence
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-22

Query Match 62.98; Score 22; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLELYR 6
DB 2 SFLEYR 7

RESULT 3
US-08-105-416-36
; Sequence 36, Application US/08105416
; Patent No. 5639958
; GENERAL INFORMATION:
; APPLICANT: Olsson, Lennart
; APPLICANT: Goodenow, Robert S
; APPLICANT: Goldstein, Avram
; TITLE OF INVENTION: Class I MHC Modulation of Surface
; TITLE OF INVENTION: Receptor Activity
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,416
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A55115-4/BIR
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-105-416-36

Query Match 57.18; Score 20; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLELY 5
DB 3 TLELY 7

RESULT 4
US-08-473-656A-36
; Sequence 36, Application US/08473656A
; Patent No. 5839999
; GENERAL INFORMATION:
; APPLICANT: Olsson, Lennart
; APPLICANT: Goodenow, Robert S
; APPLICANT: Goldstein, Avram
; TITLE OF INVENTION: Class I MHC Modulation of Surface
; TITLE OF INVENTION: Receptor Activity
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,656A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/105,416
; FILING DATE: 12-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I.
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A55115-4/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-473-656A-36

Query Match 57.18; Score 20; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TLELY 5
DB 3 TLELY 7

RESULT 5
US-09-020-880-78
; Sequence 78, Application US/09020880A
; Patent No. 6136558
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ballinger, Marcus D.
; APPLICANT: Jones, Jennifer T.
; APPLICANT: Fairbrother, Wayne J.
; APPLICANT: Sliwowski, Mark X.
; APPLICANT: Wells, James A.
; TITLE OF INVENTION: HERGULIN VARIANTS
; FILE REFERENCE: 14918-720CON1
; CURRENT APPLICATION NUMBER: US/09/020,880A
; CURRENT FILING DATE: 1998-02-09

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:50:47 ; Search time 25.72 Seconds
(without alignments)
39.810 Million cell updates/sec

Title: US-09-281-760c-4
Perfect score: 35
Sequence: 1 TULEYRM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 65

Immun DB seq length: 0
Immun DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Hit No.	Score	Query Match	Length	DB	ID	Description
1	13	37.1	7	12	Q9Y010	Q9Y010 porcine tira
2	10	28.6	5	13	P82071	P82071 litorea rub
3	10	28.6	5	13	P82072	P82072 litorea rub
4	10	28.6	7	2	054248	054248 streptomyc
5	8	22.9	6	4	008720	008720 homo sapien
6	8	22.9	7	8	098865	098865 spiniacia ol
7	8	22.9	7	8	099182	099182 gnatholebia
8	8	22.9	7	12	066205	066205 porcine tira
9	7	20.0	7	2	P72081	P72081 nocardia la
10	7	20.0	7	2	050556	050556 actinobacil
11	7	20.0	7	4	015897	015897 homo sapien
12	7	20.0	7	6	028742	028742 cryptocolagus
13	7	20.0	7	8	P92421	P92421 pathyrostia
14	7	20.0	7	8	P92385	P92385 hordeum mar
15	7	20.0	7	8	P92210	P92210 agropyron c
16	7	20.0	7	8	P92214	P92214 amblyopyrum
17	7	20.0	7	8	P92218	P92218 australopyr
18	7	20.0	7	8	P92221	P92221 bromus iner
19	7	20.0	7	8	P92226	P92226 crithopsis

20	7	20.0	7	8	P92372	P92372 haynaldia v
21	7	20.0	7	8	P92381	P92381 hordeum bra
22	7	20.0	7	8	P92387	P92387 henrardla p
23	7	20.0	7	8	P92390	P92390 heteranthel
24	7	20.0	7	8	P92393	P92393 hordeum vul
25	7	20.0	7	8	P92425	P92425 pseudoroegn
26	7	20.0	7	8	P92427	P92427 peridictyon
27	7	20.0	7	8	P92430	P92430 aegilops ta
28	7	20.0	7	8	P92442	P92442 taeniathe
29	7	20.0	7	8	P92440	P92440 thnopyrum
30	7	20.0	7	8	P92403	P92403 lophopyrum
31	7	20.0	7	12	Q9YVE3	Q9YVE3 human adeno
32	7	20.0	7	12	Q9YIR0	Q9YIR0 human adeno
33	7	20.0	7	12	Q9YIQ9	Q9YIQ9 human adeno
34	7	20.0	7	13	P82065	P82065 litorea rub
35	7	20.0	7	13	P82101	P82101 litorea rub
36	6	17.1	4	11	008433	008433 rattus norv
37	6	17.1	5	13	P82070	P82070 litorea rub
38	6	17.1	5	13	P82100	P82100 litorea rub
39	6	17.1	7	2	Q34028	Q34028 pseudomonas
40	6	17.1	7	2	P70804	P70804 azotobacter
41	6	17.1	7	8	Q95945	Q95945 saccharomyc
42	6	17.1	7	10	P82445	P82445 nicotiana t
43	6	17.1	7	12	Q66113	Q66113 cherry leaf
44	5	14.3	5	10	Q99007	Q99007 hordeum vul
45	5	14.3	5	13	P82073	P82073 litorea rub
46	5	14.3	5	13	P82099	P82099 litorea rub
47	5	14.3	6	10	P82181	P82181 spiniacia ol
48	5	14.3	6	10	P82182	P82182 spiniacia ol
49	5	14.3	6	10	P82541	P82541 spiniacia ol
50	5	14.3	6	13	P82096	P82096 litorea rub

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	7 AA.
ID	Q9Y010			
AC	Q9Y010;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	HYPOTHETICAL FUSION PROTEIN.			
OS	Porcine transmissible gastroenteritis virus.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;			
OX	NCBI_TaxID=11149;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99099045; PubMed=9882359;			
RA	Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Piana-Duran J.,			
RA	Enjuanes L.;			
RT	"Replication and packaging of transmissible gastroenteritis			
RT	coronavirus-derived synthetic minigenomes.";			
RL	J. Virol. 73:1535-1545(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95159435; PubMed=7856095;			
RA	Elcouet J., Rassaert D., Lambert P., Levy L., Vende P., Laude H.;			
RT	"Complete sequence (20 kilobases) of the polypeptide-encoding gene 1			
RT	of transmissible gastroenteritis virus.";			
RL	Virology 206:817-822(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88078100; PubMed=2825819;			
RA	Rassaert D., Gelfi J., Laude H.;			
RT	"Enteric coronavirus NSG: partial sequence of the genomic RNA, its			
RT	organization and expression.";			
RL	Biochimie 69:591-600(1987).			
DR	EMBL; AJ011482; CAA09625.1;			
SO	SEQUENCE 7 AA: 927 MW; 69D6D7273B5726F0 CRC64;			

Query Match 37.1%; Score 13; DB 12; Length 7;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEY 5
 DB 4 LQOF 7

RESULT 2
 ID P82071 PRELIMINARY; PRT; 5 AA.

AC P82071. PRELIMINARY; PRT; 5 AA.
 DT 01-MAY-2000 (TREMELREL. 13, Created)
 DT 01-MAY-2000 (TREMELREL. 13, Last sequence update)
 DE 01-MAY-2000 (TREMELREL. 13, Last annotation update)
 DE RUBELIDIN 2.1.
 OS Litoria rubella (Desert tree frog)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Steinborner S.T., Mablitz P.A., Maugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTI-BIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAH.
 CC KW Amphibian skin.
 SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 28.6%; Score 10; DB 13; Length 5;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 LEY 5
 DB 1 IEF 3

RESULT 3
 ID P82072 PRELIMINARY; PRT; 5 AA.

AC P82072. PRELIMINARY; PRT; 5 AA.
 DT 01-MAY-2000 (TREMELREL. 13, Created)
 DT 01-MAY-2000 (TREMELREL. 13, Last sequence update)
 DE 01-MAY-2000 (TREMELREL. 13, Last annotation update)
 DE RUBELIDIN 3.1.
 OS Litoria rubella (Desert tree frog)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Steinborner S.T., Mablitz P.A., Maugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTI-BIOTIC ACTIVITY.

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAH.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 28.6%; Score 10; DB 13; Length 5;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 LEY 5
 DB 1 IEF 3

RESULT 4
 ID O54248 PRELIMINARY; PRT; 7 AA.

AC O54248. PRELIMINARY; PRT; 7 AA.
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DE 01-NOV-1996 (TREMELREL. 01, Last annotation update)
 DE SECT 6 ADR GENES (FRAGMENT).
 GN RPLD.
 OS Streptomyces griseus.
 OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-N2-3-11;
 RA Poshling S., Piepersberg W., Weinzier U.F.;
 RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; X95915; CAA65160.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 28.6%; Score 10; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 TILE 4
 DB 2 TYTE 5

RESULT 5
 ID O08720 PRELIMINARY; PRT; 6 AA.

AC O08720. PRELIMINARY; PRT; 6 AA.
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DE 01-NOV-1996 (TREMELREL. 08, Last annotation update)
 DE Y PROTEIN (FRAGMENT).
 GN CREB.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93010691; PubMed=1396344;
 RA Weber G., Habener J.F.;
 RT "Novel testis germ cell-specific transcript of the CREB gene contains
 RT an alternatively spliced exon with multiple in-frame stop codons.";
 RL Endocrinology 131:2010-2015(1992).
 DR EMBL; X68994; CAA48780.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:51:12 ; Search time 10.46 Seconds
(without alignments)
24.537 Million cell updates/sec

Title: US-09-281-760c-4
Perfect score: 35
Sequence: 1 TILLEYRM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 50 summaries

Database : Swissprot_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	34.3	6	ASP2_LACSN	P82655 lactobacilli
2	12	34.3	7	FAR2_ASCSU	P31890 ascaris suu
3	10	28.6	6	OVN_LEPDE	P42985 leptinotars
4	10	28.6	7	CCFL_ENTFA	P20104 enterococcu
5	9	25.7	7	HY7_PIG	P01153 sus scrofa
6	8	22.9	6	FARP_MONEX	P41966 moniezia ex
7	8	22.9	7	FAR5_ASCSU	P31889 ascaris suu
8	8	22.9	7	GFRP_MOUSE	P39025 mus musculu
9	8	22.9	7	MSCL_SALTY	P39446 salmoneilla
10	8	22.9	4	FAR3_HIRME	P42562 hirudo medi
11	7	20.0	4	FAR4_HIRME	P42563 hirudo medi
12	7	20.0	4	FIRF_HIRME	P42561 hirudo medi
13	7	20.0	4	FAR4_CARMA	P81817 carclnus ma
14	7	20.0	5	FARP_AKTRR	P81853 artiposthi
15	7	20.0	5	PRCT_PERAM	P01373 periplaneta
16	7	20.0	5	PSK_DAUCA	P58261 daucus caro
17	7	20.0	6	ACPH_RABIT	P2154 oryctolagus
18	7	20.0	7	ALL2_CARMA	P81805 carclnus ma
19	7	20.0	7	ALL3_CARMA	P81806 carclnus ma
20	7	20.0	7	ALL4_CARMA	P81807 carclnus ma
21	7	20.0	7	ALL5_CARMA	P81808 carclnus ma
22	7	20.0	7	ALL7_CYPDO	P82158 cydia pomon
23	7	20.0	7	CARP_MYTED	P81420 mytilus edu
24	7	20.0	7	FAR1_HELTI	P41871 helisma tr
25	7	20.0	7	FAR1_PROCT	P34999 procambarus
26	7	20.0	7	FAR2_PROCT	P38498 procambarus
27	7	20.0	7	FAR3_HABCO	P81298 haemochnus
28	7	20.0	7	FAR3_PANRE	P41874 panagrellus
29	7	20.0	7	NMP1_LEPDE	P42984 leptinotars
30	7	20.0	7	MYOM_APICA	P15153 aplysia cal
31	7	20.0	7	UN06_PINS	P81675 pinus pinas
32	7	20.0	7	WMA1_ACHFU	P35919 achatina fu
33	7	20.0	7		

34	6	17.1	6	1	TMOF_SARBU	P41495 sarcophaga
35	6	17.1	7	1	CIA_ENTFA	P11932 enterococcu
36	6	17.1	7	1	LANC_CARUI	P36960 carnobacter
37	6	17.1	7	1	UE03_MOUSE	P38641 mus musculu
38	5	17.1	7	1	WMA2_ACHFU	P35920 achatina fu
39	5	14.3	4	1	DCML_PSECH	P19916 pseudomonas
40	5	14.3	4	1	DCMS_PSECH	P19918 pseudomonas
41	5	14.3	4	1	EOSI_HUMAN	P02731 homo sapien
42	5	14.3	4	1	FMRF_MACNT	P01162 macrocallis
43	5	14.3	4	1	RM01_YEAST	P36515 saccharomyc
44	5	14.3	4	1	TUPT_HUMAN	P01858 homo sapien
45	5	14.3	5	1	BIOA_CITFR	P13071 citrobacter
46	5	14.3	5	1	BIOA_SALTY	P12677 salmoneilla
47	5	14.3	5	1	BIOB_CITFR	P12997 citrobacter
48	5	14.3	5	1	BIOB_SALTY	P12678 salmoneilla
49	5	14.3	5	1	TRM3_ECOLI	P13873 escherichia
50	5	14.3	5	1	UC22_MAI2E	P80628 zea mays (m

ALIGNMENTS

RESULT 1
ASP2_LACSN STANDARD: PRT: 6 AA.
AC P82655;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ACID SHOCK PROTEIN 2 (FRAGMENT).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=CBL.
RX PubMed-11429463;
RA De Angelis M., Bini L., Pallini V., Coccocelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBL.";
RL Microbiology 147:1863-1873(2001).
FT -1- INDUCTION: OVEREXPRESSED IN ACID ENVIRONMENTS.
SQ SEQUENCE 6 AA: 778 MW: 6AA5B5B132A8000 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 Ey 5
DB 3 Ey 4

RESULT 2
FAR2_ASCSU STANDARD: PRT: 7 AA.
AC P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253; 6233;
RN [1]
RP SEQUENCE.
RC SPECIES=A.suum;
RX MEDLINE=93324431; PubMed=8332542;
RA Cowden C., Stretton A.O.W.;

"AF2, an Ascaris neuropeptide: Isolation, sequence, and bioactivity.";
 RL Peptides 14:423-430(1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P. redivivus;
 RX MEDLINE-95060998; PubMed-7970891;
 RA Maule A.G., Shaw C., Bowman J.W.;
 RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the
 free-living nematode, Panagrellus redivivus (Nematoda, Rhabditidae).";
 RL Parasitology 109:351-356(1994).
 CC - FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
 CC - TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC - SIMILARITY: BELONGS TO THE FMRF (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 AA; 992 MW; 69D4073B5B11E350 CRC64;
 SQ SEQUENCE

Query Match 34.3%; Score 12; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 EY 5
 Db 3 EY 4

RESULT 3
 OVM_LEPDE STANDARD: PRT: 6 AA.
 ID AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE OVIDUCTAL MOTILITY STIMULATING PEPTIDE (LED-OVM).
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Coleoptera; Chrysomelidae; Polyphaga;
 OC Cuculiformia; Phytophaga; Chrysomelidae; Chrysomelidae;
 OC Chrysomelinae; Leptinotarsa.
 CX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE. AND SYNTHESIS.
 RC TISSUE-Head;
 RX MEDLINE-91271080; PubMed-2052497;
 RA Spittels K, Schoofs L., Grauwels L., Smet H., van Damme J.,
 Proost P., Torrekens S., de Loof A.;
 RT "Isolation, identification and synthesis of novel oviductal motility
 stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 decemlineata";
 RL Peptides 12:31-36(1991).
 CC - FUNCTION: MOTILITIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC - OVIDUCT.
 KW Neuropeptide; Amidation.
 FT MOD_RES 6 AA; 720 MW; 6B07632B5D03000 CRC64;
 SQ SEQUENCE

Query Match 28.6%; Score 10; DB 1; Length 6;
 Best Local Similarity 25.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LEYR 6
 Db 1 IAYK 4

RESULT 4
 CCFL_ENTFA STANDARD: PRT: 7 AA.
 ID CCFL_ENTFA
 AC P20104;

DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE SEX PHEROMONE CCF10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 CX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-89008113; PubMed-1139658;
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 Adelt J.C., Dunny G.M., Suzuki A.;
 RT "Structure of CCF10, a peptide sex pheromone which induces
 conjugative transfer of the Streptococcus faecalis tetracycline
 resistance plasmid, pCF10";
 RL J. Biol. Chem. 263:14574-14578(1988).
 CC - FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC - PIR. A30812; A30812.
 KW Pheromone.
 FT MOD_RES 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
 SQ SEQUENCE

Query Match 28.6%; Score 10; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TL 3
 Db 3 TLV 5

RESULT 5
 HY7_PIG STANDARD: PRT: 7 AA.
 ID AC P01153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE HYPOTHALAMIC HEPTAPEPTIDE.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE. AND SYNTHESIS.
 RX MEDLINE-81213980; PubMed-6263778;
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
 Saffrin M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
 RT "Isolation, structure and synthesis of a heptapeptide with in vitro
 ACH-releasing activity from porcine hypothalamus";
 RL Horm. Metab. Res. 13:228-232(1981).
 CX PIR. A01417; NTPG7.
 FT MOD_RES 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
 SQ SEQUENCE

Query Match 25.7%; Score 9; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+05; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 YR 6
 Db 6 YK 7

RESULT 6
 FARP_MONEX STANDARD: PRT: 6 AA.
 ID FARP_MONEX
 AC P41966;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:49:07 ; Search time 19.61 Seconds
(without alignments)
27.191 Million cell updates/sec

Title: US-09-281-760C-4
Perfect score: 35
Sequence: 1 TILLEYM 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 455

Minimum DB seq length: 0
Minimum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR.68:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	45.7	7	2 S25266	PILE protein - Esc
2	13	37.1	5	2 S69237	surface protein te
3	13	37.1	6	2 I37027	protamine P1 - gor
4	13	37.1	7	2 S71867	glutathione transi
5	12	34.3	3	2 A22565	R-phycocerythrin al
6	12	34.3	5	2 B37325	pap fibribrial regul
7	12	34.3	5	2 F22565	R-phycocerythrin ga
8	12	34.3	6	2 A41946	T-cell receptor ga
9	12	34.3	7	2 A38081	amine oxidase (cop
10	12	34.3	7	2 I56595	hypothetical L2 pr
11	11	31.4	6	2 T11779	phosphoglycerate t
12	11	31.4	7	2 S71870	glutathione transi
13	11	31.4	7	2 B34818	vicillin 57k chain
14	10	28.6	5	2 I40469	dnazX-like protein
15	10	28.6	6	2 S11556	hydrogensulfite re
16	10	28.6	7	2 A30812	sex pheromone ccfl
17	9	25.7	3	2 A43391	TRH-like tripeptid
18	9	25.7	3	2 T13892	cytochrome-c oxida
19	9	25.7	4	2 E44823	synaprosomal-assoc
20	9	25.7	5	2 E42364	flagellar protein
21	9	25.7	6	2 S68326	blood cell protein
22	9	25.7	6	2 S11024	hydrogensulfite re
23	9	25.7	6	2 B44510	hypothetical prote
24	9	25.7	6	2 A43766	28k ubiquitin-immu
25	9	25.7	6	2 I65546	neuropeptide TR-6
26	9	25.7	6	2 I65546	MAC H-2 antigen
27	9	25.7	7	1 N1P67	hypothalamic hepta
28	9	25.7	7	2 JN0859	peptidyl dipeptida
29	9	25.7	7	2 S78024	ribosomal protein

30	8	22.9	4	2 A37832	phenol 2-monooxyge
31	8	22.9	4	2 I61883	protamine P1 - ora
32	8	22.9	4	2 I37013	protamine P1 - Cer
33	8	22.9	4	2 I84439	protamine P1 - sav
34	8	22.9	5	2 I39964	ribosomal protein
35	8	22.9	5	2 I39966	ribosomal protein
36	8	22.9	5	2 I39965	ribosomal protein
37	8	22.9	5	2 P00689	photosystem I 10.4
38	8	22.9	5	2 A44692	fulicin - giant Af
39	8	22.9	6	2 A60986	N-formyl oligopept
40	8	22.9	6	2 I37263	Y protein - human
41	8	22.9	6	2 B56979	collagen alpha 1(I
42	8	22.9	6	2 H48394	glycoprotein compo
43	8	22.9	6	2 I49808	D-SP2.5 region - m
44	8	22.9	6	2 B39322	Ig mu chain D regi
45	8	22.9	6	2 I49424	cytotoxic T-lympho
46	8	22.9	6	2 I49421	lamnin B1 - weste
47	8	22.9	6	2 A43129	neuropeptide GNFR
48	8	22.9	7	2 S20446	elastase - Pseudom
49	8	22.9	7	2 S17976	glucose isomerase
50	8	22.9	7	2 A34026	acetylcholinestera

ALIGNMENTS

RESULT 1
S25266
PILE protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 11-Jun-1993
C:Accession: S25266
R:Dupuy, B.; Taha, M.R.; Possot, O.; Marchal, C.; Pugsley, A.P.
Mol. Microbiol. 6, 1887-1894, 1992
A>Title: Pili, a component of the pullulanase secretion pathway of Klebsiella oxytoca
A:Reference number: S25266; MUID:92374839
A:Accession: S25266
A:Molecule type: protein
A:Residues: 1-7 <DUP>
A:Genetics:
A:Gene: PILE

Query Match 45.7% Score 16; DB 2; Length 7;
Best Local Similarity 75.0% Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TILIE 4
||:|
Db 2 TILIE 5

RESULT 2
S69237
surface protein tetrahedron heavy chain - Staphylothermus marinus (fragment)
C:Species: Staphylothermus marinus
C>Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Peterson, J.; Nitsch, M.; Kuehlmoorgen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Eng
J. Mol. Biol. 245, 385-401, 1995
A>Title: Tetrahedron: a filamentous archaeobacterial surface protein assembly of unu
A:Reference number: S69237; MUID:95139068
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <PET>
A:Experimental source: strain FL, DSM 3639
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 37.1% Score 13; DB 2; Length 5;
Best Local Similarity 100.0% Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TLL 3
|||
DB 2 TLL 4

RESULT 3

I37027
Protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralt, R.; Oliva, R.
Genes I33, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-enc
A:Reference number: I37013; MUID: 94040810
A:Accession: I37027
A:Status: Preliminary: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:212145; NID:922910; PIDN:CAW8129.1; PID:9579612

Query Match 37.1%; Score 13; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LLEY 6
|||
DB 1 MAKYR 5

RESULT 4

S71867
glutathione transferase (EC 2.5.1.18) class alpha 5 - pig (fragment)
N:Alternate names: glutathione S-transferase class alpha 5
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S71867
R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrosp
A:Reference number: S71864; MUID: 96332484
A:Accession: S71867
A:Molecule type: Protein
A:Residues: 1-7 <ROU>
C:Comment: At least five species-independent classes of cytosolic glutathion transferase
A:Mitochondrial form are known.
C:Complex: dimer
C:Function:
A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
A:Pathway: detoxification; xenobiotics metabolism
A:Note: Increased hydrophilicity of GSH-conjugates facilitates their further metabolism
C:Superfamily: glutathione transferase
C:Keywords: dimer; transferase

Query Match 37.1%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 LLEY 5
|||
DB 2 ILNY 5

RESULT 5

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID: 85182601
A:Accession: A22565
A:Molecule type: Protein
A:Residues: 1-3 <KLO>

Query Match 34.3%; Score 12; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 YR 6
|||
DB 2 YR 3

RESULT 6

B37325
pap fibribial regulatory protein papI - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C:Accession: B37325
R:Bratzen, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.
J. Bacteriol. 173, 1789-1800, 1991
A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus
A:Reference number: A37325; MUID: 91154136
A:Accession: B37325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <BRA>
A:Cross-references: GB:M63747

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 EY 5
|||
DB 3 EY 4

RESULT 7

F22565
R-phycoerythrin gamma-A chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID: 85182601
A:Accession: F22565
A:Molecule type: Protein
A:Residues: 1-5 <KLO>

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 YR 6
|||
DB 4 YR 5

RESULT 8

A41946
T-cell receptor gamma chain (1t.22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A41946

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 21, 2002, 10:43:21 ; Search time 12.87 Seconds
(without alignments)
13.988 Million cell updates/sec

Title: US-09-281-760C-3

Perfect score: 24

Sequence: 1 LXXYRXLI 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents_AA:*

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	58.3	5	2	US-08-968-676-25
2	14	58.3	6	2	US-08-968-676-24
3	14	58.3	7	2	US-08-968-676-22
4	14	58.3	7	4	US-09-273-565-60
5	14	58.3	7	4	US-09-139-802-140
6	14	58.3	8	1	US-08-335-198-11
7	14	58.3	8	2	US-08-968-676-21
8	14	58.3	8	4	US-08-160-604-117
9	14	58.3	8	4	US-08-160-604-116
10	13	54.2	7	4	US-09-142-078-31
11	13	54.2	7	4	US-09-357-141-31
12	12	50.0	2	4	US-09-214-614-2
13	12	50.0	3	2	US-08-968-676-27
14	12	50.0	4	1	US-08-240-712-4
15	12	50.0	4	1	US-08-428-488-59
16	12	50.0	4	1	US-08-428-488-60
17	12	50.0	4	1	US-08-428-488-61
18	12	50.0	4	1	US-08-428-488-62
19	12	50.0	4	1	US-08-428-488-63
20	12	50.0	4	1	US-08-428-488-64
21	12	50.0	4	1	US-08-428-488-65
22	12	50.0	4	1	US-08-428-488-66
23	12	50.0	4	1	US-08-428-488-67
24	12	50.0	4	1	US-08-428-488-68
25	12	50.0	4	1	US-08-428-488-69
26	12	50.0	4	1	US-08-428-488-70
27	12	50.0	4	1	US-08-428-488-71

28	12	50.0	4	1	US-08-428-488-72	Sequence 72, Appl
29	12	50.0	4	1	US-08-428-488-73	Sequence 73, Appl
30	12	50.0	4	1	US-08-428-488-74	Sequence 74, Appl
31	12	50.0	4	1	US-08-255-272-22	Sequence 22, Appl
32	12	50.0	4	1	US-08-335-198-25	Sequence 25, Appl
33	12	50.0	4	1	US-08-429-732-20	Sequence 20, Appl
34	12	50.0	4	1	US-08-203-8068-15	Sequence 15, Appl
35	12	50.0	4	1	US-08-443-890-4	Sequence 4, Appl
36	12	50.0	4	1	US-08-706-178-2	Sequence 2, Appl
37	12	50.0	4	2	US-08-441-871-1	Sequence 1, Appl
38	12	50.0	4	2	US-08-441-871-63	Sequence 63, Appl
39	12	50.0	4	2	US-08-441-871-65	Sequence 65, Appl
40	12	50.0	4	2	US-08-441-871-66	Sequence 66, Appl
41	12	50.0	4	2	US-08-441-871-68	Sequence 68, Appl
42	12	50.0	4	2	US-08-441-871-70	Sequence 70, Appl
43	12	50.0	4	2	US-08-473-022-2	Sequence 2, Appl
44	12	50.0	4	2	US-08-705-660-27	Sequence 27, Appl
45	12	50.0	4	2	US-08-705-660-28	Sequence 28, Appl
46	12	50.0	4	2	US-08-623-8338-61	Sequence 61, Appl
47	12	50.0	4	2	US-08-685-589A-6	Sequence 6, Appl
48	12	50.0	4	2	US-08-685-589A-62	Sequence 62, Appl
49	12	50.0	4	2	US-08-968-676-26	Sequence 26, Appl
50	12	50.0	4	2	US-08-752-844-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-968-676-25
Sequence 25, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS: 165
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968, 676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-25

Query Match 58.3%; Score 14; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 YRXXL 8
| | |
Db 1 YRMKL 5

RESULT 2

US-08-968-676-24

Sequence 24 Application US/08968676
Patent No. 5919639

GENERAL INFORMATION:

APPLICANT: Humphreys, Robert E

APPLICANT: Adams, Shariene

TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell, P.C.

STREET: P.O. Box 999

STATE: ME

COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/968,676

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: REH-9601

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0558

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-968-676-24

OY 4 YRXXL 8
| | |
Db 1 YRMKL 5

RESULT 3

US-08-968-676-22

Sequence 22 Application US/08968676
Patent No. 5919639

GENERAL INFORMATION:

APPLICANT: Humphreys, Robert E

APPLICANT: Adams, Shariene

TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kevin M. Farrell, P.C.

STREET: P.O. Box 999

CITY: York Harbor

STATE: ME
COUNTRY: USA

ZIP: 03911

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/968,676

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Farrell, Kevin M

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: REH-9601

TELECOMMUNICATION INFORMATION:

TELEPHONE: (207) 363-0558

TELEFAX: (207) 363-0558

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-968-676-22

OY 4 YRXXL 8
| | |
Db 1 YRMKL 5

RESULT 4

US-09-273-565-60

Sequence 60 Application US/09273565A
Patent No. 6166190

GENERAL INFORMATION:

APPLICANT: FUJIMURA, TSUTOMU

APPLICANT: MATSUMOTO, TAKESHI

APPLICANT: HORIE, MASARU

TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN

FILE REFERENCE: Q-353599

CURRENT APPLICATION NUMBER: US/09/273,565A

EARLIER FILING DATE: 1997-03-22

EARLIER FILING DATE: 1997-03-22

EARLIER FILING DATE: 1998-04-07

EARLIER FILING DATE: 1997-03-19

EARLIER FILING DATE: 1996-03-19

EARLIER FILING DATE: 1997-03-05

NUMBER OF SEQ ID NOS: 95

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO: 60

LENGTH: 7

TYPE: PRT

ORGANISM: Bovine sp.

US-09-273-565-60

OY 4 YRXXL 8
| | |
Db 1 YRMKL 5

Query Match 58.3%; Score 14; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LXXR 5

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:39:31 ; Search time 26.36 Seconds
(without alignments)
22.481 Million cell updates/sec

Title: US-09-281-760C-3

Perfect score: 24

Sequence: 1 LXXYRXRL 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 62388

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

A.Genesec_1101.*
1: /SIDSI/gcgdata/geneseq/AA1980.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	16	66.7	8	21	AAV69583
5	15	62.5	6	19	AAW59001
6	15	62.5	7	21	AAV51949
7	15	62.5	8	22	AAV75743
8	14	58.3	5	2	AAV10205
9	14	58.3	5	11	AAV08321
10	14	58.3	5	15	AAV5499
11	14	58.3	5	15	AAV5508

12	14	58.3	5	15	AAV55490
13	14	58.3	5	19	AAV47949
14	14	58.3	5	21	AAV69581
15	14	58.3	5	21	AAV69582
16	14	58.3	6	7	AAV60150
17	14	58.3	6	16	AAV83527
18	14	58.3	6	19	AAV50982
19	14	58.3	6	19	AAV58989
20	14	58.3	6	19	AAV59000
21	14	58.3	6	19	AAV47948
22	14	58.3	6	20	AAV84425
23	14	58.3	7	11	AAV06424
24	14	58.3	7	13	AAV24585
25	14	58.3	7	13	AAV24664
26	14	58.3	7	19	AAV60423
27	14	58.3	7	19	AAV47946
28	14	58.3	7	20	AAV42007
29	14	58.3	7	20	AAV42072
30	14	58.3	7	20	AAV93750
31	14	58.3	7	21	AAV21840
32	14	58.3	7	21	AAV69584
33	14	58.3	7	21	AAV50878
34	14	58.3	7	22	AAV15373
35	14	58.3	7	22	AAV15358
36	14	58.3	7	22	AAV06418
37	14	58.3	7	22	AAV62830
38	14	58.3	7	22	AAV03292
39	14	58.3	7	22	AAV31715
40	14	58.3	8	6	AAV51212
41	14	58.3	8	18	AAV24920
42	14	58.3	8	19	AAV47945
43	14	58.3	8	20	AAV4654
44	14	58.3	8	20	AAV47418
45	14	58.3	8	21	AAV10411
46	14	58.3	8	21	AAV67357
47	14	54.2	5	22	AAV81468
48	13	54.2	6	19	AAV87348
49	13	54.2	6	19	AAV87354
50	13	54.2	6	19	AAV87342

ALIGNMENTS

RESULT 1	AAV34076	standard; peptide; 7 AA.
ID	AAV34076	
XX	AAV34076	
AC	AAV34076	
XX	23-NOV-1999	(first entry)
DT	XX	
DE	Bacteroides 100 kba antigen peptide fragment.	
XX	XX	
KW	Ulcerative colitis; histone; H1-like antigen; porin antigen; Bacteroides antigen; inflammatory bowel disease; IBD; PANCA; perinuclear anti-neutrophil cytoplasmic antibody; diagnosis.	
XX	XX	
OS	Bacteroides cacciae.	
XX	XX	
PN	WO945955-A1.	
XX	XX	
PD	16-SEP-1999.	
XX	XX	
PF	12-MAR-1999; 99WO-0505492.	
XX	XX	
PR	12-MAR-1998; 98US-0041889.	
XX	XX	
PA	(REGC) UNIV CALIFORNIA.	
XX	XX	
PI	Braun J, Cohavy O;	
XX	XX	
DR	WPI; 1999-551215/46.	

Opioid oligopeptid
AE101 analogue eff
Generic immunogeni
Human growth hormo
Zif268 zinc finger
Growth hormone rel
Human HLA-B27 pept
Human HLA-B27 pept
AE101 analogue eff
HIV-1 nucleic acid
Peptide with delta
Immunomodulatory p
Immunomodulatory p
Tumour homing pept
AE101 analogue eff
Rheumatoid arthritis
Rheumatoid arthritis
Mouse B16B15b meia
Murine melanoma ho
Immunogenic peptid
Antibody 8H.8 bind
Schizophrenia-asso
Schizophrenia-asso
Tumour homing pept
Amino acid sequenc
Fruit fly G proteol
Peptide with argin
Analgesic peptide.
Vesicular stomatit
AE101 analogue eff
Immunogenic peptid
Immunogenic peptid
T cell epitope/MHC
Melanoma glycoprot
Synthetic peptide,
Peptide determined
Peptide determined
Peptide determined

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:45:41 ; Search time 25.75 Seconds
(without alignments)
45.444 Million cell updates/sec

Title: US-09-281-760c-3
Perfect score: 24
Sequence: 1 LXXYRXXL 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Minimum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SPTREMBL_17:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	58.3	8	2	052062	052062 bacillus me
2	12	50.0	8	2	09R9C2	09R9C2 borrellia me
3	12	50.0	8	2	09GDA7	09GDA7 hyalastetele
4	12	50.0	8	8	09GCD00	09GCD00 masoala mad
5	12	50.0	8	8	09GCZ4	09GCZ4 nenga pumil
6	10	41.7	7	8	09G182	09G182 gnatholebia
7	10	41.7	8	5	P82618	P82618 periplaneta
8	9	37.5	7	8	098866	098866 spinacia ol
9	9	37.5	8	4	09GMM9	09GMM9 homo sapien
10	9	37.5	8	8	035792	035792 saccharomyc
11	8	33.3	7	2	050556	050556 actinodacil
12	8	33.3	8	2	009258	009258 synechococc
13	8	33.3	8	2	045889	045889 clostridium
14	8	33.3	8	2	09ZIE9	09ZIE9 neisseria m
15	8	33.3	8	2	09R049	09R049 buchnera ap
16	8	33.3	8	8	019958	019958 gossypium b
17	8	33.3	8	8	019956	019956 gossypium a
18	8	33.3	8	8	019959	019959 gossypium t
19	8	33.3	8	8	019960	019960 gossypium m

20	8	33.3	8	8	019961	019961 gossypium d
21	8	33.3	8	8	09XNP8	09XNP8 boophilus m
22	8	33.3	8	10	P83324	P83324 pisum sativ
23	8	33.3	8	11	09ERD2	09ERD2 mus musculu
24	7	29.2	7	12	09YVE3	09YVE3 human adeno
25	7	29.2	7	12	09Y010	09Y010 porcine tra
26	7	29.2	7	12	09Y1R0	09Y1R0 human adeno
27	7	29.2	7	12	09Y1Q9	09Y1Q9 human adeno
28	7	29.2	7	13	P82065	P82065 litorea rub
29	7	29.2	7	13	P82101	P82101 litorea rub
30	7	29.2	8	2	P72221	P72221 pseudomonas
31	7	29.2	8	2	085406	085406 coxiella bu
32	7	29.2	8	2	09S443	09S443 pseudomonas
33	7	29.2	8	2	09R057	09R057 buchnera ap
34	7	29.2	8	2	09R7T2	09R7T2 escherichia
35	7	29.2	8	2	09R5R2	09R5R2 shigella dy
36	7	29.2	8	3	P87225	P87225 saccharomyc
37	7	29.2	8	4	015888	015888 homo sapien
38	7	29.2	8	4	015890	015890 homo sapien
39	7	29.2	8	4	015898	015898 homo sapien
40	7	29.2	8	4	09U750	09U750 homo sapien
41	7	29.2	8	4	09UHK1	09UHK1 homo sapien
42	7	29.2	8	4	09UD24	09UD24 homo sapien
43	7	29.2	8	4	09BYT5	09BYT5 homo sapien
44	7	29.2	8	5	09TWH6	09TWH6 periteneis
45	7	29.2	8	6	09BFC3	09BFC3 didelphis m
46	7	29.2	8	6	09BFC2	09BFC2 macropus eu
47	7	29.2	8	6	09BFC1	09BFC1 choleopus h
48	7	29.2	8	6	09BFC0	09BFC0 choleopus d
49	7	29.2	8	6	09BFB9	09BFB9 euphractus
50	7	29.2	8	6	09BFB8	09BFB8 chaetophirac

ALIGNMENTS

RESULT 1
ID 052062 PRELIMINARY; PRT: 8 AA.
AC 052062;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE SIGMA FACTOR (FRAGMENT).
GN SPOTTGB.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Fawcett P., Melnikov A., Youngman P.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017181; AAB94056.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA: 1057 MW: F0DA00441BA1ADD6 CRC64;

Query Match 58.3%; Score 14; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 4,7e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXYR 5
DB 1 MAYR 5
RESULT 2
ID 09R9C2 PRELIMINARY; PRT: 8 AA.
AC 09R9C2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE PLASMID CP32-3, POSSIBLE PARTITION PROTEINS, COMPLETE CDS (FRAGMENT).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid cp32-3.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B31;
 RX MEDLINE=98361033; PubMed=9695920;
 RA Stevenson B., Casjens S., Rosa P.;
 RT "Evidence of past recombination events among the genes encoding the
 RT Etp antigens of Borrelia burgdorferi.";
 RL Microbiology 144:0-0(0).
 DR EMBL; AF022480; AAC35445.1; -.
 KW Plasmid
 FT NON_TER
 SQ SEQUENCE 8 AA; 985 MW; EBB41B41A735B446 CRC64;

Query Match 50.0%; Score 12; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 4 YR 5
 DB 6 YR 7

RESULT 3
 ID 09GD47 PRELIMINARY; PRT; 8 AA.
 AC 09GD47;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE RIBOSOMAL PROTEIN S16 (FRAGMENT).
 GN RPS16
 OS Hydrolyase microspadix.
 OG Chloroplast
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Hydrocharitaceae;
 OX NCBI_TaxID=112711;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Asmusen C.B., Chase M.W.;
 RT "Coding and noncoding plastid DNA in palm systematics.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ404943; CAC17895.1; -.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 975 MW; 9236C2C0441B505D CRC64;

Query Match 50.0%; Score 12; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 4 YR 5
 DB 3 YR 4

RESULT 4
 ID 09GD00 PRELIMINARY; PRT; 8 AA.
 AC 09GD00;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE RIBOSOMAL PROTEIN S16 (FRAGMENT).

GN RPS16.
 OS Masoala madagascariensis.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Masoala.
 OX NCBI_TaxID=131286;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Asmusen C.B., Chase M.W.;
 RT "Coding and noncoding plastid DNA in palm systematics.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ404949; CAC17925.1; -.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 916 MW; 9D71E735A41B505D CRC64;

Query Match 50.0%; Score 12; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 4 YR 5
 DB 3 YR 4

RESULT 5
 ID 09GC24 PRELIMINARY; PRT; 8 AA.
 AC 09GC24;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE RIBOSOMAL PROTEIN S16 (FRAGMENT).
 GN RPS16.
 OS Nenga pumila.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Areaceae; Nenga.
 OX NCBI_TaxID=131288;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Asmusen C.B., Chase M.W.;
 RT "Coding and noncoding plastid DNA in palm systematics.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ404944; CAC18505.1; -.
 KW Chloroplast.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 975 MW; 9236C2C0441B505D CRC64;

Query Match 50.0%; Score 12; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

OY 4 YR 5
 DB 3 YR 4

RESULT 6
 ID 099182 PRELIMINARY; PRT; 7 AA.
 AC 099182;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 GN COI.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:46:07 ; Search time 10.34 Seconds
(without alignments)
28.367 Million cell updates/sec

Title: US-09-281-760c-3
Perfect score: 24
Sequence: 1 LXXYRXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	10	41.7	8 1 ALI6_CYPDPO	P82157 cydia pomon
2	10	41.7	8 1 UPAA_HUMAN	P30096 homo sapien
3	9	37.5	6 1 OVA_LEPDE	P42985 lepidoptars
4	9	37.5	7 1 HY7_PIG	P01153 sus scrofa
5	9	37.5	8 1 ALI1_CYPDPO	P82152 cydia pomon
6	9	37.5	8 1 COXG_RAT	P80430 rattus norv
7	8	33.3	5 1 ALI4_CARMA	P81817 carcius ma
8	8	33.3	6 1 FARP_MONEX	P41966 moniezia ex
9	8	33.3	7 1 ALI2_CARMA	P81805 carcius ma
10	8	33.3	7 1 ALI3_CARMA	P81806 carcius ma
11	8	33.3	7 1 ALI5_CARMA	P81807 carcius ma
12	8	33.3	7 1 ALI5_CARMA	P81808 carcius ma
13	8	33.3	7 1 NMP1_LEPDE	P42984 lepidoptars
14	8	33.3	8 1 ALI2_CARMA	P81815 carcius ma
15	8	33.3	8 1 ALI5_CARMA	P81818 carcius ma
16	8	33.3	8 1 ALI6_CARMA	P81819 carcius ma
17	8	33.3	8 1 ALI7_CARMA	P81820 carcius ma
18	8	33.3	8 1 ALI8_CARMA	P81821 carcius ma
19	8	33.3	8 1 ALI3_CYPDPO	P82154 cydia pomon
20	8	33.3	8 1 ALI4_CALVO	P41840 calliphora
21	8	33.3	8 1 ALI4_CYPDPO	P82155 cydia pomon
22	8	33.3	8 1 ALI7_CARMA	P81809 carcius ma
23	8	33.3	8 1 ALI8_CARMA	P81811 carcius ma
24	8	33.3	8 1 ALI9_CARMA	P81812 carcius ma
25	8	33.3	8 1 B44K_PORCI	P81886 porphyromon
26	7	29.2	4 1 FARP3_HIRME	P42562 hitudo medi
27	7	29.2	4 1 FARP4_HIRME	P42563 hitudo medi
28	7	29.2	5 1 FARP_AKTRR	P41873 periplaneta
29	7	29.2	5 1 PRCT_PERAM	P01373 periplaneta
30	7	29.2	5 1 PSK_DAVCA	P58261 daucus caro
31	7	29.2	6 1 ACPH_RABIT	P25154 oryctolagus
32	7	29.2	6 1 ASP2_LACSN	P82655 lactobacill
33	7	29.2	7 1 ALI7_CYPDPO	P82158 cydia pomon

34	7	29.2	7 1 FARP1_PROCL	P38499 procambarrus
35	7	29.2	7 1 FARP2_ASCSU	P31890 ascatis suu
36	7	29.2	7 1 FARP2_PROCL	P38498 procambarrus
37	7	29.2	7 1 FARP3_HAECO	P81298 haemonphus
38	7	29.2	7 1 FARP3_PANRE	P41874 panagrellus
39	7	29.2	7 1 FARP5_HIRME	P42564 hitudo medi
40	7	29.2	7 1 GERP_MOUSE	P99025 mus musculu
41	7	29.2	7 1 UN06_PINPS	P81675 pinus pinas
42	7	29.2	7 1 WMA1_ACFPU	P35919 achatina fu
43	7	29.2	7 1 AKH_MELML	P25423 melolontha
44	7	29.2	8 1 ALI5_CALVO	P41841 calliphora
45	7	29.2	8 1 ALI5_CYPDPO	P82156 cydia pomon
46	7	29.2	8 1 ANG2_BOTJA	Q10582 bothrops ja
47	7	29.2	8 1 CCKN_MACEU	P30369 macropus eu
48	7	29.2	8 1 FARP3_HOMAM	P41486 homarus ame
49	7	29.2	8 1 FARP4_HOMAM	P41487 homarus ame
50	7	29.2	8 1 LCK8_LEUMA	P19950 leucophaea

ALIGNMENTS

RESULT 1	ALI6_CYPDPO	STANDARD:	PRT:	8 AA.
ID	ALI6_CYPDPO			
AC	P82157;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	CYDIASTATIN 6.			
OS	Cydia pomonella (codling moth).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;			
OC	Tortricidae; Tortricidae; Olethreutinae; Cydia.			
OX	NCBI_TaxID=82600;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Larva;			
RX	MEDLINE=98054539; PubMed=9392829;			
RA	Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,			
RA	Dave M., East P.D., Thorpe A.;			
RT	Lepidopteran peptides of the allatostatin superfamily.";			
RL	Peptides 18:1301-1309(1997).			
CC	-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.			
KM	Neuropeptide; Amidation.			
FT	MOD.RES 8			
FT	SEQUENCE 8 AA; 936 MW; OB2879C45B573767 CRC64;			
QY	1 LXXYRXXL 8			
Db	1 LPLYNEGL 8			
Query Match	41.7%; Score 10; DB 1; Length 8;			
Best Local Similarity	37.5%; Pred. No. 1e+05;			
Matches 3; Conservative	0; Mismatches 5; Indels 0; Gaps 0;			
RESULT 2	UPAA_HUMAN	STANDARD:	PRT:	8 AA.
ID	UPAA_HUMAN			
AC	P30096;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 36) (FRAGMENT).			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Plasma;			

RX MEDLINE-93092937; PubMed1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing";
 CC Electrophoresis 13:707-714(1992)
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 7. ITS MW IS: 12 KDa.
 DR SWISS-2DPAGE: p30096; HUMAN.
 FT NON_TER
 FT VARIANT 5 5 F->P /FTID=VAR_000004.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA: 909 MW: 86677B59D1A72042 CRC64;

Query Match 41.7%; Score 10; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXY 4
 DB 3 LFY 6

RESULT 3
 OVM_LEPDE STANDARD; PRT; 6 AA.
 ID ID
 AC P42985;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE OVIDUCTAL MOTILITY STIMULATING PEPTIDE (LED-OVM).
 DE Leptinotarsa decemlineata (Colorado potato beetle).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cuculiformia; Phyllophaga; Chrysomelidae; Chrysomelidae;
 CC Chrysomelinae; Leptinotarsa.
 CC NCBI_TaxID=7539;
 OX [1]
 RN SEQUENCE. AND SYNTHESIS.
 RP TISSUE-Head;
 RC MEDLINE-91271080; PubMed-2052497;
 RA Spittels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
 RA Proost P., Torrekens S., de Loof A.;
 RT "Isolation, identification and synthesis of novel oviductal motility
 RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
 RT decemlineata";
 RT Peptides 12:31-36(1991).
 CC -1- FUNCTION: MITOCHONDRIAL PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC -1- OVIDUCT.
 CC Neuropeptide; Amidation.
 KW MOD_RES 6 6 AMIDATION.
 FT MOD_RES 6 6
 FT SEQUENCE 6 AA: 720 MW: 6B07632B5D03000 CRC64;

Query Match 37.5%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YR 5
 DB 3 YK 4

RESULT 4
 HY7_PIG STANDARD; PRT; 7 AA.
 ID ID
 AC P01153;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE HIPOTHALAMIC HEPTAPEPTIDE.

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE. AND SYNTHESIS.
 RX MEDLINE-81213980; PubMed-6263778;
 RA Chang R.C.C., Huang W.-Y., Atimira A., Redding T.W., Coy D.H.,
 RA Salitra M., Kong A., Hamilton J.W., Com D.V., Schally A.V.;
 RT Isolation, structure and synthesis of a heptapeptide with in vitro
 RT ACTH-releasing activity from porcine hypothalamus.;
 RL Horm. Metab. Res. 13:228-232(1981).
 RL FIR, A01417; NPG.
 SQ SEQUENCE 7 AA: 957 MW: 632B45B1FB5059A0 CRC64;

Query Match 37.5%; Score 9; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YR 5
 DB 6 YK 7

RESULT 5
 ALL1_CYDPO STANDARD; PRT; 8 AA.
 ID ID
 AC P82152;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYDIASTATIN 1.
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diurysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 CC NCBI_TaxID=82600;
 OX [1]
 RN SEQUENCE.
 RP TISSUE-larva;
 RC MEDLINE-98054539; PubMed-9392829;
 RA Dure H., Jonsson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Tholpe A.;
 RT "Lepidopteran peptides of the allostatin superfamily.";
 RT Peptides 18:1301-1309(1997).
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8 8 AMIDATION.
 FT MOD_RES 8 8
 FT SEQUENCE 8 AA: 934 MW: C82B79C45B51F775 CRC64;

Query Match 37.5%; Score 9; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YRXL 8
 DB 4 YNFG 8

RESULT 6
 COXG_RAT STANDARD; PRT; 8 AA.
 ID ID
 AC P80430;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1) (AED) (FRAGMENT).
 CN COX6B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:43:41 ; Search time 19.59 Seconds
(Without alignments)
31.108 Million cell updates/sec

Title: US-09-281-760C-3
Perfect score: 24
Sequence: 1 LXXYRXXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR 68: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	54.2	6	2	137027
2	12	50.0	3	2	A22565
3	12	50.0	5	2	R22565
4	12	50.0	6	2	A41946
5	12	50.0	7	4	I56695
6	12	50.0	8	2	PT0030
7	9	37.5	6	2	S11556
8	9	37.5	6	2	A11490
9	9	37.5	6	2	B56979
10	9	37.5	7	1	NYP67
11	9	37.5	8	2	S63493
12	9	37.5	8	2	S68802
13	9	37.5	8	2	S16324
14	9	37.5	8	2	S65381
15	8	33.3	4	2	I61883
16	8	33.3	4	2	I37013
17	8	33.3	4	2	I84439
18	8	33.3	5	2	B57325
19	8	33.3	5	2	I39964
20	8	33.3	5	2	I39966
21	8	33.3	5	2	I39965
22	8	33.3	5	2	I40469
23	8	33.3	6	2	I49421
24	8	33.3	6	2	A43129
25	8	33.3	7	2	S55548
26	8	33.3	8	2	B27867
27	8	33.3	8	2	D47393
28	7	29.2	3	2	A43391
29	7	29.2	3	2	S68328

30	7	29.2	4	2	A32039	tyrosine-melanocyt
31	7	29.2	4	2	A37832	phenol 2-monooxyge
32	7	29.2	4	2	S09478	globulin IV alpha
33	7	29.2	4	2	PT0240	Ig heavy chain CRD
34	7	29.2	5	1	S43959	Ig mu chain V regi
35	7	29.2	5	1	H0R0HA	proctolin - Americ
36	7	29.2	5	2	F60274	major protein anti
37	7	29.2	5	2	P00009	angiotensin-conver
38	7	29.2	5	2	P00689	photosystem I 10.4
39	7	29.2	5	2	B61445	Leu-enkephalin - b
40	7	29.2	5	2	A61445	Met-enkephalin - b
41	7	29.2	5	2	A60411	proctolin - Atlant
42	7	29.2	5	2	PT0278	Ig heavy chain CRD
43	7	29.2	5	2	S68326	blood cell protein
44	7	29.2	5	4	A58728	serrawetin W2 - S
45	7	29.2	6	2	JN0861	peptidyl-dipeptida
46	7	29.2	6	2	A61411	amelatin - rat
47	7	29.2	6	2	A35890	RNA-directed DNA p
48	7	29.2	6	2	B44510	hypothetical prote
49	7	29.2	6	2	A49792	acylaminoacyl-pept
50	7	29.2	6	2	F41946	T-cell receptor ga

ALIGNMENTS

RESULT 1
137027
protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: 137027
R:Queral, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: 137013; MUID:94040810
A:Accession: 137027
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:212145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 54.2% Score 13; DB 2; Length 6;
Best Local Similarity 40.0% Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LXXYR 5
: 11
DB 1 MARYR 5

RESULT 2
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 50.0% Score 12; DB 2; Length 3;
Best Local Similarity 100.0% Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 YR 5
11

Db 2 YR 3

RESULT 3

F22565 R-phycocerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: F22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycocerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: F22565

A:Molecule type: protein

A:Residues: 1-5 <K10>

Db 4 YR 5

RESULT 4

T-cell receptor gamma chain (1t.22) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: A41946

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g

A:Reference number: A41946; MUID:92049316

A:Accession: A41946

A:Molecule type: DNA

A:Residues: 1-6 <MHC>

A:Keywords: T-cell receptor

Db 4 YR 5

RESULT 5

hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (fragment)

C:Species: human papillomavirus type 16

C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: I56695

R:Schneider-Maunoury, S.; Croissant, O.; Orth, G.

J. Virol. 61, 3295-3298, 1987

A:Title: Integration of human papillomavirus type 16 DNA sequences: a possible early eve

A:Reference number: I56695; MUID:87111896

A:Accession: I56695

A:Status: translated from GB/EMBL/DBD

A:Molecule type: DNA

Query Match 50.0%; Score 12; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YR 5

Db 1 YR 2

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YR 5

Db 3 YR 4

RESULT 6

inulinase (EC 3.2.1.7) - Aspergillus ficum (fragment)

N:Alternate names: inulase

C:Species: Aspergillus ficum

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999

C:Accession: P10030

R:Etalib, M.; Baratti, J.C.

Agric. Biol. Chem. 54, 61-68, 1990

A:Title: Molecular and kinetic properties of Aspergillus ficum inulinases.

A:Reference number: P10030; MUID:90344234

A:Accession: P10030

A:Molecule type: protein

A:Residues: 1-8 <ERR>

A:Keywords: glycosidase; hydrolase; polysaccharide degradation

QY 4 YR 5

Db 7 YR 8

RESULT 7

hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragmen

N:Alternate names: disulfite reductase; desulfosulfidn

C:Species: Desulfovibrio thermophilus

C:Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998

C:Accession: S11556

R:Faucu, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.J.G.

Biochim. Biophys. Acta 1040, 112-118, 1990

A:Title: Purification and characterization of disulfite reductase (desulfosulfidn) f

A:Reference number: S11024; MUID:90335276

A:Accession: S11556

A:Molecule type: protein

A:Residues: 1-6 <FAU>

A:Keywords: oxidoreductase

QY 4 YR 5

Db 5 YR 6

RESULT 8

pyruvate kinase (EC 2.7.1.40) - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995

C:Accession: A11490

R:Hjeltnist, G.; Andersson, J.; Edlund, B.; Engstrom, L.

Biochem. Biophys. Res. Commun. 61, 559-563, 1974

A:Title: Amino acid sequence of a (132-P)phosphopeptide from pig liver pyruvate kinase

A:Reference number: A11490; MUID:75127438

A:Accession: A11490

A:Molecule type: protein

A:Residues: 1-6 <HJE>

Query Match 37.5%; Score 9; DB 2; Length 6;

Best Local Similarity 50.0%; Pred. No. 2.2e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 21, 2002, 10:15:59 ; Search time 94.43 Seconds
(without alignments)
2.621 Million cell updates/sec

Title: US-09-281-760C-5
Perfect score: 63
Sequence: 1 GNNLFWYRESK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA: *
1: /cgn2_6/pdata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/pdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/pdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/pdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/pdata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/pdata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	63	100.0	426	1	US-08-336-583-2	Sequence 2, Appl1
2	63	100.0	426	5	PCT-US95-13795-2	Sequence 2, Appl1
3	41	65.1	583	2	US-08-432-016-2	Sequence 2, Appl1
4	41	65.1	583	2	US-08-684-594-2	Sequence 2, Appl1
5	38	60.3	107	4	US-09-240-274-46	Sequence 46, Appl1
6	38	60.3	256	2	US-08-481-905-113	Sequence 113, App
7	38	60.3	256	3	US-08-481-985B-113	Sequence 113, App
8	38	60.3	256	4	US-08-370-476-113	Sequence 113, App
9	38	60.3	500	4	US-08-960-190A-25	Sequence 25, Appl
10	37	58.7	860	1	US-08-117-362-3	Sequence 3, Appl1
11	37	58.7	860	1	US-08-486-924-3	Sequence 3, Appl1
12	37	58.7	894	1	US-08-117-362-4	Sequence 4, Appl1
13	37	58.7	894	1	US-08-486-924-4	Sequence 4, Appl1
14	36	57.1	96	1	US-08-276-852-113	Sequence 113, App
15	36	57.1	96	1	US-08-899-575-113	Sequence 113, App
16	36	57.1	96	1	US-08-899-575-113	Sequence 113, App
17	36	57.1	96	5	PCT-US95-08743-113	Sequence 113, App
18	36	57.1	128	4	US-08-569-147-74	Sequence 74, Appl
19	36	57.1	182	2	US-08-417-495-25	Sequence 25, Appl
20	36	57.1	182	2	US-08-284-391B-25	Sequence 25, Appl
21	36	57.1	182	2	US-09-218-950-25	Sequence 25, Appl
22	36	57.1	182	5	PCT-US92-01785-25	Sequence 25, Appl
23	36	57.1	182	5	PCT-US95-00454-25	Sequence 25, Appl
24	36	57.1	750	6	5457037-3	Patent No. 5457037
25	36	57.1	751	6	5457037-5	Patent No. 5457037
26	36	57.1	772	2	US-08-410-784A-5	Sequence 5, Appl1
27	36	57.1	776	4	US-09-346-237-4	Sequence 4, Appl1

28	36	57.1	776	4	US-09-346-237-7	Sequence 7, Appl1
29	35	55.6	110	1	US-08-497-312-29	Sequence 29, Appl
30	35	55.6	110	1	US-08-497-312-31	Sequence 31, Appl
31	35	55.6	246	4	US-09-113-750A-34	Sequence 34, Appl
32	35	55.6	319	3	US-08-413-118-119	Sequence 119, App
33	35	55.6	319	3	US-08-473-446-119	Sequence 119, App
34	35	55.6	391	5	PCT-US95-15696-2	Sequence 2, Appl
35	35	55.6	459	1	US-08-220-151-12	Sequence 12, Appl
36	35	55.6	459	1	US-08-220-151-14	Sequence 14, Appl
37	35	55.6	459	1	US-08-413-118-12	Sequence 12, Appl
38	35	55.6	459	1	US-08-413-118-14	Sequence 14, Appl
39	35	55.6	459	3	US-08-473-446-112	Sequence 12, Appl
40	35	55.6	459	3	US-08-473-446-14	Sequence 14, Appl
41	35	55.6	459	4	US-09-213-053-6	Sequence 4, Appl1
42	35	55.6	661	1	US-08-514-014-4	Sequence 4, Appl1
43	35	55.6	661	2	US-08-833-823-4	Sequence 4, Appl1
44	35	55.6	668	1	US-08-232-538-13	Sequence 13, Appl
45	35	55.6	668	2	US-08-786-164-13	Sequence 13, Appl
46	35	55.6	714	2	US-08-990-114-3	Sequence 3, Appl1
47	35	55.6	767	2	US-08-874-678-2	Sequence 2, Appl1
48	35	55.6	767	3	US-08-643-833-2	Sequence 2, Appl1
49	35	55.6	788	1	US-08-232-538-15	Sequence 15, Appl
50	35	55.6	788	2	US-08-786-164-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-336-583-2
Sequence 2, Application US/08336583
Patent No. 5629415
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2
Query Match 100.0%; Score 63; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMLTWYRESK 11
|||||
DB 245 GMLTWYRESK 255

L X X Y R

RESULT 2
PCT-US95-13795-2
Sequence 2, Application PC/TUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 100.0%; Score 63; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GMLTWYRESK 11
|||||
DB 245 GMLTWYRESK 255
RESULT 3
US-08-432-016-2
Sequence 2, Application US/08432016
Patent No. 5968768
GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA

COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,016
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: Xaa = W/S
OTHER INFORMATION: Xaa = W/T
US-08-432-016-2

Query Match 65.1%; Score 41; DB 2; Length 583;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 NLTWYRESK 11
|:|||||
DB 167 NLTWYRESK 175

RESULT 4
US-08-684-594-2
Sequence 2, Application US/08684594
Patent No. 5998172
GENERAL INFORMATION:
APPLICANT: HAYNES, BARTON F.
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: PATEL, DHAVALKUMAR
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: MARQUARDT, HANS
TITLE OF INVENTION: CD6 LIGAND
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,594
FILING DATE: 18-JUL-1996

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,016
; FILING DATE: 01-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: Xaa = M/S
; OTHER INFORMATION: Xaa = M/T
US-08-684-594-2

```

```

Query Match      65.1%; Score 41; DB 2; Length 583;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      3 NLTWYRESK 11
Db      167 NITWYRNSK 175

```

```

RESULT 5
US-09-240-274-46
; Sequence 46, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RND-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I16
US-09-240-274-46

```

```

Query Match      60.3%; Score 38; DB 4; Length 107;
Best Local Similarity 50.0%; Pred. No. 7.5;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY      1 GMLTWYRES 10
Db      29 GMLTWYRES 38

```

```

RESULT 6
US-08-484-905-113
; Sequence 113, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS-/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 03495.0106-03000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-113

```

```

Query Match      60.3%; Score 38; DB 2; Length 256;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY      2 NLTWYRESK 11
Db      144 INITWYRNSK 153

```

```

RESULT 7
US-08-481-985B-113
; Sequence 113, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-113

Query Match 60.3%; Score 38; DB 3; Length 256;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 MNLWYRESK 11
Db 144 INITWLRNSK 153

RESULT 8
US-08-370-476-113
Sequence 113; Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Moltez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-113

Query Match 60.3%; Score 38; DB 4; Length 256;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 MNLWYRESK 11
Db 144 INITWLRNSK 153

RESULT 9
US-08-960-190A-25
Sequence 25; Application US/08960190A
Patent No. 6232445
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Cui, Jia, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: usa
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSFO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F.
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-960-190A-25

Query Match 60.3%; Score 38; DB 4; Length 500;
Best local similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 MNTWYRESK 11
:|:|:|:|:|
Db 388 INITWLRNSK 397

RESULT 10
US-08-117-362-3
Sequence 3, Application US/08117362
Patent No. 5595872
GENERAL INFORMATION:
APPLICANT: Wettlerau II, John R.
APPLICANT: Sharp, Daru Y.
TITLE OF INVENTION: MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,362
FILING DATE: 03-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC21b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-5901
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 860 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-117-362-3

Query Match 58.7%; Score 37; DB 1; Length 860;
Best local similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYRESK 11
|:|:|:|:|
Db 736 WYRESK 741

RESULT 11
US-08-486-924-3
Sequence 3, Application US/08486924
Patent No. 5789197
GENERAL INFORMATION:
APPLICANT: Wettlerau II, John R.
APPLICANT: Sharp, Daru Y.
TITLE OF INVENTION: MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,924
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,362
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
REFERENCE/DOCKET NUMBER: DC21b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-5901
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 860 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-924-3

Query Match 58.7%; Score 37; DB 1; Length 860;
Best local similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYRESK 11
|:|:|:|:|
Db 736 WYRESK 741

RESULT 12
US-08-117-362-4
Sequence 4, Application US/08117362
Patent No. 5595872
GENERAL INFORMATION:
APPLICANT: Wettlerau II, John R.
APPLICANT: Sharp, Daru Y.
TITLE OF INVENTION: MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESS: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,362
FILING DATE: 03-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: DC21b
TELEPHONE: (609) 252-5901
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-117-362-4

Query Match 58.7%; Score 37; DB 1; Length 894;
Best Local Similarity 100.0%; Pred. No. 1,2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYRESK 11
DB 770 WYRESK 775

RESULT 13
US-08-486-924-4
Sequence 4, Application US/08486924
Patent No. 5789197
GENERAL INFORMATION:
APPLICANT: Welterau II, John R.
APPLICANT: Sharp, Daru Y.
APPLICANT: Gregg, Richard E.
TITLE OF INVENTION: MICROSOFT TRIGLYCERIDE TRANSFER PROTEIN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burton Rodney
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,924
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,362
FILING DATE: 03-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION NUMBER: 33,111

REFERENCE/DOCKET NUMBER: DC21b
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-5901
TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-924-4

Query Match 58.7%; Score 37; DB 1; Length 894;
Best Local Similarity 100.0%; Pred. No. 1,2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WYRESK 11
DB 770 WYRESK 775

RESULT 14
US-08-276-852-113
Sequence 113, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Barbas, Carlos F.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-113

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Clark & Elbing LLP
;; STREET: 176 Federal Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/284,391B
;; FILING DATE: 02-AUG-1994
;;
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/195,395
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: 07/847,566
;; FILING DATE: 06-MAR-1992
;; APPLICATION NUMBER: 07/665,961
;; FILING DATE: 07-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elbing, Karen L
;; REGISTRATION NUMBER: 35,238
;; REFERENCE/DOCKET NUMBER: 00786/247001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-428-0200
;; TELEFAX: 617-428-7045
;; TELEX:
;;
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 182 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-284-391B-25

Query Match 57.1%; Score 36; DB 2; Length 182;
Best Local Similarity 44.4%; Pred. No. 30;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 NITWYRESK 11
|:|:|:|:|
Db 52 NITWFKDKG 60

ULT 21
09-218-950-25
; Sequence 25, Application US/09218950
; Patent No. 6284240
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian
; APPLICANT: Banapour, Babak
; APPLICANT: Romeo, Charles
; APPLICANT: Kolanus, Waldemar
; TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
; TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR-BEARING CELLS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSeq for Windows Version 2.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/218,950
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/284,391
;; FILING DATE: 02-AUG-1994
;; APPLICATION NUMBER: 08/195,395
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: 07/847,566
;; FILING DATE: 06-MAR-1992
;; APPLICATION NUMBER: 07/665,961
;; FILING DATE: 07-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elbing, Karen L
;; REGISTRATION NUMBER: 35,238
;; REFERENCE/DOCKET NUMBER: 00786/247001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-428-0200
;; TELEFAX: 617-428-7045
;; TELEX:
;;
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 182 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-09-218-950-25

Query Match 57.1%; Score 36; DB 4; Length 182;
Best Local Similarity 44.4%; Pred. No. 30;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 NITWYRESK 11
|:|:|:|:|
Db 52 NITWFKDKG 60

RESULT 22
PCT-US92-01785-25
; Sequence 25, Application PC/TUS9201785
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor
; TITLE OF INVENTION: Chimeras
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/01785
; FILING DATE: 19920306
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/665,961
; FILING DATE: March 7, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/119002
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: amino acid
PCT-US95-01785-25

Query Match 57.1%; Score 36; DB 5; Length 182;
Best Local Similarity 44.4%; Pred. No. 30;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 NLTWYRESK 11
|:|:|:|
b 52 NITWFKDQK 60

RESULT 23
PCT-US95-00454-25
Sequence 25, Application PC/TUS9500454
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Targeted Cytolysis of HIV-Infected
CELLS BY CHIMERIC CD4 RECEPTOR-
TITLE OF INVENTION: Beating Cells
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Morpheus (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00454
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acid
PCT-US95-00454-25

Query Match 57.1%; Score 36; DB 5; Length 182;
Best Local Similarity 44.4%; Pred. No. 30;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 3 NLTWYRESK 11
|:|:|:|
Db 52 NITWFKDQK 60

RESULT 24
5457037-3
Patent No. 5457037
APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
GALLI, GIULIANO;LUCCHESI, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOMYLASE
ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/1,797
FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 749,621
FILING DATE: 19-AUG-1991
APPLICATION NUMBER: 224,114
FILING DATE: 25-JUL-1988
SEQ ID NO:3:
LENGTH: 750
5457037-3

Query Match 57.1%; Score 36; DB 6; Length 750;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GNNLTWYRES 10
|:|:|:|
Db 640 GSQLTWYQPS 649

RESULT 25
5457037-5
Patent No. 5457037
APPLICANT: TOGNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
GALLI, GIULIANO;LUCCHESI, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLO
TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOMYLASE
ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/1,797
FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 749,621
FILING DATE: 19-AUG-1991
APPLICATION NUMBER: 224,114
FILING DATE: 25-JUL-1988
SEQ ID NO:5:
LENGTH: 751
5457037-5

Query Match 57.1%; Score 36; DB 6; Length 751;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GNNLTWYRES 10
|:|:|:|
Db 641 GSQLTWYQPS 650

Search completed: April 21, 2002, 10:16:00
Job time: 285 sec

